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96753

From: McGarry, Sean
Sent: Tuesday, June 17, 2003 10:12 AM
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Subject: SEQ SEARCH 09/964,666

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JUN 17 2003

(STIC)

Sean McGarry 73484
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305-7028

09/964,666

Please, a length limited (nt \leq 50) search of SEQ ID NOS 9-14.

Thank You

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 6/17/03
Date Completed: 6/23/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 10
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 01
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 522.031 Seconds

(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26

Sequence: 1 TGTGTCATGCTTGTGTCACAGCTAC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_din:*
35: em_hlg_fod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.2	62.3	21	6	AX050293
2	16	61.5	50	6	AX199678
3	15.6	60.0	47	6	AX378267
4	15.2	58.5	20	6	AR067246
5	15.2	58.5	21	6	AX117706
6	15.2	58.5	27	6	AX429427
7	15	57.7	27	6	AX116084
8	15	57.7	28	6	AR164904
9	15	57.7	44	6	AR116815
10	14.8	56.9	36	6	AR023949
11	14.8	56.9	36	6	II12127
12	14.8	56.9	36	6	II15450
13	14.8	56.9	36	6	II1297
14	14.4	55.4	20	6	I31358
15	14.4	55.4	41	6	I32222
16	14.2	54.6	19	6	AX010420
17	14.2	54.6	42	6	AR022354
18	14	53.8	31	6	AX248371
19	14	53.8	31	6	AX249312
20	14	53.8	33	6	AX405134
21	14	53.8	37	6	AX477864
22	14	53.8	45	9	HS4224254
23	13.8	53.1	34	6	AX184141
24	13.8	53.1	37	6	AX040679
25	13.8	53.1	42	6	AX173376
26	13.6	52.3	24	6	AX291119
27	13.6	52.3	31	6	AX249648
28	13.6	52.3	38	6	AR078070
29	13.6	52.3	38	6	E35651
30	13.6	52.3	39	6	AR078068
31	13.6	52.3	39	6	AR098737
32	13.6	52.3	39	6	E35649
33	13.6	52.3	39	6	E35696
34	13.4	51.5	17	6	AR171891
35	13.4	51.5	21	6	AR169512
36	13.4	51.5	25	6	AX476156
37	13.4	51.5	25	6	AX476157
38	13.4	51.5	25	6	AX476158
39	13.4	51.5	30	6	I89866
40	13.4	51.5	31	6	BD002550
41	13.4	51.5	32	6	AX234354
42	13.4	51.5	35	6	AR040575
43	13.4	51.5	35	6	AR055599
44	13.4	51.5	37	6	AX223015
45	13.4	51.5	39	6	AR040576

ALIGNMENTS

RESULT 1
AX050293 21 bp DNA linear PAT 12-JAN-2001
LOCUS Sequence 47 from Patent WO0070046.
DEFINITION AX050293
ACCESSION AX050293
VERSION AX050293.1 GI:12226574
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 21)
AUTHORS Shimkets,R.A., Fernandes,E. and Boldog,F.
TITLE Secreted polypeptides and corresponding polynucleotides
JOURNAL Patent: WO 0070046-A 47 23-NOV-2000;
Curagen Corporation (US)

FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically synthesized"
BASE COUNT 4 a 7 c 5 g 5 t
ORIGIN

Query Match 62.3%; Score 16.2; DB 6; Length 21;
Best Local Similarity 85.7%; Pred. No. 1.2e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 GCATGCTTTGGTCCAGCTA 25
||||| ||| |||||
Db 1 GCATGCTGTAGTCCAGCTA 21

RESULT 2
AX199678/c AX199678 50 bp DNA linear PAT 29-AUG-2001
LOCUS Sequence 608 from Patent W00151670.
DEFINITION AX199678
ACCESSION AX199678
VERSION AX199678.1 GI:15390118
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shinkens,R.A. and Leach,M.D.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0151670-A 608 19-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature 25..26
/note="Nucleotide deleted between bases 25 and 26"
Accession number cg44129408"
misc-feature 26
/note="2 of 2 allelic variants (607 is other entry)"
BASE COUNT 14 a 12 c 11 g 13 t
ORIGIN

Query Match 61.5%; Score 16; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 1.4e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 3 GTGCATGCTTTGGTCCAGCTAC 26
||||| ||| |||||
Db 26 GCGCATGCCTGTATCCAGCTAC 3

RESULT 3
AX378267/c AX378267 47 bp DNA linear PAT 18-MAR-2002
LOCUS Sequence 56 from Patent W00206525.
DEFINITION AX378267
ACCESSION AX378267
VERSION AX378267.1 GI:19574117
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
TITLE Obesity associated biallelic marker maps
JOURNAL Patent: WO 0206525-A 56 24-JAN-2002;
GENSET (FR)
FEATURES Location/Qualifiers
source 1..47

variation
BASE COUNT 9 a 20 c 10 g 7 t 1 others
ORIGIN

Query Match 60.0%; Score 15.6; DB 6; Length 47;
Best Local Similarity 75.0%; Pred. No. 2.2e+04;
Matches 18; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGGTCATGCTTTGGTCCAGCT 24
||||| ||| |||||
Db 40 TAGTCATGCTTACAGYCCAGCT 17

RESULT 4
AR067246/c AR067246 20 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 594 from patent US 5851760.
DEFINITION AR067246
ACCESSION AR067246
VERSION AR067246.1 GI:5998468
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Evans,G.A. and Smith,M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 594 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 5 a 3 c 9 g 3 t
ORIGIN

Query Match 58.5%; Score 15.2; DB 6; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 ATGCTTTGGTCCAGCTAC 26
||||| ||| |||||
Db 20 ATCCCTGTGTCAGCTAC 1

RESULT 5
AX117706/c AX117706 21 bp DNA linear PAT 11-MAY-2001
LOCUS Sequence 2829 from Patent W00129262.
DEFINITION AX117706
ACCESSION AX117706
VERSION AX117706.1 GI:14034657
KEYWORDS
SOURCE synthetic construct;
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 21)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2829 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES Location/Qualifiers
source 1..21
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
BASE COUNT 5 a 4 c 7 g 5 t
ORIGIN

Query Match 58.5%; Score 15.2; DB 6; Length 21;
Best Local Similarity 85.0%; Pred. No. 3.7e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 ATGCTTTGGTCCAGCTAC 26

BASE COUNT 4 a /organism="unknown"
ORIGIN 12 c 14 g 11 t

Query Match 55.48; Score 14.4; DB 6; Length 41;
Best Local Similarity 75.08; Pred. No. 8e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 GTGCATGTCTTGGTCCAGCTAC 26
 |||| | | | | | | | | | |
DB 7 GTCCGAGGCTGTGGGCCCACTAC 30

Search completed: June 21, 2003, 22:14:28
Job time : 527.031 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 142.594 Seconds
(without alignments)
410.621 Million cell updates/sec

Title: US-09-964-666-10
Perfect score: 26
Sequence: 1 TGTGCGATGCTTTGTGCCAGCTAC 26

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq_101002:.*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:.*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:.*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:.*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:.*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:.*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:.*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:.*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:.*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:.*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:.*
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15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:.*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:.*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:.*
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22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:.*
25: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	67.7	31	20	AA06149
2	17.2	66.2	33	24	ABL40961
3	16.2	62.3	21	22	AA023445
4	16	61.5	50	22	AA089827
5	15.6	60.0	47	24	ABK40808
6	15.2	58.5	20	16	AA082594
7	15.2	58.5	21	22	AA040033
8	15.2	58.5	27	24	ABK92971
9	15.2	58.5	36	21	AAA35578

C	10	15.2	58.5	50	22	AA131378	Human SNP oligonuc
C	11	15	57.7	27	22	AA038411	SNP specific SNPE
C	12	15	57.7	28	21	AA029014	Mahogany protein 9
C	13	15	57.7	44	20	AA036190	Intronic location
C	14	15	57.7	50	22	AA029684	Human SNP oligonuc
C	15	14.8	56.9	41	24	ABN87593	Oligodendrocyte-my
C	16	14.4	55.4	31	22	AA065953	Primer #2 to ampli
C	17	14.4	55.4	20	18	AA129962	Human single nucle
C	18	14.4	55.4	31	22	AA130903	Human single nucle
C	19	14.4	55.4	41	16	AA091982	FSH-beta probe
C	20	14.2	54.6	19	21	AA045351	Sense PCR primer
C	21	14.2	54.6	19	21	AA039844	PCR primer 1 for t
C	22	14.2	54.6	20	20	AA090795	Human 7SL RNA spec
C	23	14.2	54.6	41	24	ABL40963	Transcription regu
C	24	14.2	54.6	41	24	ABL40964	Transcription regu
C	25	14.2	54.6	42	24	AB082843	Human protective D
C	26	14.2	54.6	48	24	AB082842	Human protective D
C	27	14.2	54.6	50	19	AA032917	Aspergillus niger
C	28	14	53.8	33	22	AA165991	Human protein asso
C	29	14	53.8	33	24	AA039460	Maize PPDK cDNA am
C	30	14	53.8	37	24	ABN89108	Human prostate spe
C	31	14	53.8	48	24	ABN72411	Streptococcus agal
C	32	13.8	53.1	34	22	AA091368	Human inflammatory
C	33	13.8	53.1	37	21	AA068148	Cystatin mutagenic
C	34	13.8	53.1	42	22	AA069299	Forward PCR primer
C	35	13.8	53.1	50	22	AA130574	Human SNP oligonuc
C	36	13.6	52.3	24	24	AB188158	Capture oligonucle
C	37	13.6	52.3	24	24	AB188159	Capture oligonucle
C	38	13.6	52.3	25	21	AA027304	Fas ligand promote
C	39	13.6	52.3	25	22	AA021322	Human MDR-1 allele
C	40	13.6	52.3	33	22	AA084200	Human cell death p
C	41	13.6	52.3	38	20	AA056322	Neisseria gonorrhoe
C	42	13.6	52.3	39	20	AA056320	Neisseria gonorrhoe
C	43	13.6	52.3	39	20	AA030271	Neisseria gonorrhoe
C	44	13.6	52.3	50	22	AA129143	Human SNP oligonuc
C	45	13.4	51.5	17	20	AA084625	PCR primer for Hum

ALIGNMENTS

RESULT 1
AA06149/c
ID AA06149 standard; DNA: 31 BP.
XX
AC AA06149;
XX
XX 31-MAR-1999 (first entry)
XX
DE Human biallelic polymorphic DNA fragment WI-17197.
XX
XX
KW Polymorphism: biallelic; paternity testing; forensic; genetic mapping;
KW phenotypic typing; medicament; disease; marker; human; ss.
XX
OS Homo sapiens.
XX
PN W09858529-A2.
XX
PD 30-DEC-1998.
XX
XX 22-JUN-1998; 98WO-US12930.
XX
XX 24-JUN-1997; 97US-0050594.
XX
XX (AFFY-) AFFYMETRIX INC.
XX
XX Beruo A, Chee M, Fan J, Lipshutz RJ;
XX WPI: 1999-080963/07.
XX
XX New nucleic acid segments containing polymorphic sites - used for,
XX e.g. detecting a disease phenotype, in forensics, paternity testing
XX or genetic mapping of phenotypic traits


```

XX Chromosome 11 (Locus D11S863) STS primer MS20-2.
DE
XX
XX sequence sampled mapping; genomic analysis; complex genome mapping;
KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
XX
XX Synthetic.
OS
XX MO9429486-A.
PN
XX
XX 22-DEC-1994.
PD
XX
XX 15-JUN-1994; 94WO-US06810.
PE
XX
XX 15-JUN-1993; 93US-0078471.
PR
XX 07-SEP-1993; 93US-0117952.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
PA
XX
XX Evans GA, Smith MW;
PI
XX
XX WPI; 1995-036508/05.
DR
XX
XX
XX Sequencing complex genomes, present as fragments in a cosmid
PT library - by sequencing end-specific nucleotides of each clone
PT then correlating with spatial relationship of cosmid, esp. for
PT mammalian chromosomes.
XX
XX
XX Example 4; Page 89; 128pp; English.
PS
XX
XX Sequences were determined from the ends of chromosome 11-specific
CC cosmid by automated sequencing without intermediate subcloning.
CC A sample of 371 DNA sequence fragments were determined and of
CC these, 277 were suitable for STS primer prediction by computer.
CC analysis (using the "primer" program available from F. Lander, MIT).
CC The STSs and cosmids were mapped by in situ hybridization, somatic
CC cell hybrid analysis or both. Using this method, 370 STSs specific
CC for human chromosome 11 were generated and most of them were
CC regionally mapped. This procedure illustrates a novel method for
CC sequencing complex genomes, designated "sequence sampled mapping".
CC The sequence sampled mapping method is useful for the completion of
CC high density sequence-based maps, and ultimately for the complete
CC sequencing of genomic DNA directly from cosmid clones.
CC See AA082001-Q82706 and AA091325-Q91358 for STS primers.
CC
XX
XX Sequence 20 BP; 5 A; 3 C; 9 G; 3 T; 0 other;
SQ
XX
XX
XX Query Match 58.5%; Score 15.2; DB 16; Length 20;
XX Best Local Similarity 85.0%; Pred. NO. 1.4e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ATGCTTTGGTCCAGCTAC 26
DB 20 ATCCCTGTGCTCCAGCTAC 1

```

```

RESULT 7
AAH40033/c
ID AAH40033 standard; DNA: 21 BP.
XX
XX AAH40033;
AC
XX
XX 14-AUG-2001 (first entry)
DT
XX
XX SNP specific upper PCR primer SEQ ID 2829.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
XX

```

```

OS Homo sapiens.
XX
XX
XX WO200129262-A2.
PN
XX
XX 26-APR-2001.
PD
XX
XX 13-OCT-2000; 2000WO-US28436.
PE
XX
XX 15-OCT-1999; 99US-0160096.
PR
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
PA
XX
XX Picoult-Newburg L, Pohl M;
PI
XX
XX WPI; 2001-290930/30.
DR
XX
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample
PT
XX
XX
XX Claim 1; Page 64; 83pp; English.
PS
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence.
CC
XX
XX Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 other;
SQ
XX
XX
XX Query Match 58.5%; Score 15.2; DB 22; Length 21;
XX Best Local Similarity 85.0%; Pred. NO. 1.4e+03;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ATGCTTTGGTCCAGCTAC 26
DB 21 ATGCTGTAGTCCAGCTAC 2

```

```

RESULT 8
ABK92971
ID ABK92971 standard; DNA: 27 BP.
XX
XX ABK92971;
AC
XX
XX 22-AUG-2002 (first entry)
DT
XX
XX Genomic analysis method PCR primer 3'DEGIS431.
DE
XX
XX Genomic analysis; PCR; primer; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO200234939-A2.
PN
XX
XX

```


PD 02-MAY-2002.
 XX 22-OCT-2001; 2001WO-CA01487.
 XX 23-OCT-2000; 2000US-0695545.
 PR (MBIF-) MBI FERMENTAS INC.
 XX Yu AHC;
 PI WPI; 2002-489951/52.
 DR
 XX Analysing a DNA sample, involves using an extension primer generated by
 PT capturing unknown DNA with an adaptor containing a class IIS
 PT restriction enzyme recognition site in an extension/amplification
 PT reaction with DNA sample -
 XX
 PS Example 1; Page 21; 79pp: English.
 CC The invention describes a method of analysing a DNA sample using
 CC ligation, digestion and extension techniques. The method is also
 CC useful for identification and analysis of unknown sequences upstream
 CC of a known region or sequence. This sequence represents a PCR primer
 CC used in analysis of sequences captured from a restriction endonuclease
 CC digest of bacterial genomic DNA.
 CC
 SQ Sequence 27 BP; 6 A; 6 C; 4 G; 8 T; 3 other;
 Query Match 58.5%; Score 15.2; DB 24; Length 27;
 Best Local Similarity 68.0%; Pred. No. 1.4e+03;
 Matches 17; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 OY 1 TGGTCATGCTTTGGTCCACGTA 25
 1 TGGTCATGCTTTGGTCCACGTA 25
 DB 1 TGGTCATGCTTTGGTCCACGTA 25
 RESULT 9
 AAA35578
 ID AAA35578 standard; DNA; 36 BP.
 AC AAA35578;
 XX
 DT 26-JUL-2000 (first entry)
 DE Permutin linker encoding nucleotide sequence FG33.
 XX
 KW Biologically-activated circularly-permuted protein; permutin; linker;
 KW permutin library generation; therapeutic property; antigen;
 KW immunotherapy; improve bio-distribution; half life; ss.
 XX
 OS Synthetic.
 KW
 PN WO200018905-A1.
 XX
 OS
 PD 06-APR-2000.
 XX
 PF 24-SEP-1999; 99WO-US20891.
 XX
 PR 25-SEP-1998; 98US-0101908.
 XX
 PA (SEAR) SEARLE & CO G D.
 PI Lee SC;
 XX
 DR WPI; 2000-293145/25.
 XX
 PT Preparation of biologically-activated circularly-permuted proteins by
 PT scanning permutagenesis for generating libraries of permutins with
 PT improved therapeutic properties -
 XX
 PS Claim 11; Page 40; 100pp: English.
 XX

CC The preparation of biologically-activated circularly-permuted proteins
 CC (permutins) comprises the use of a method comprising making a series of
 CC circularly permuted genes. The circularly permuted genes are inserted
 CC into a display vector, where they are expressed so that the proteins
 CC they encode are presented on the surface of the display vector. A library
 CC of display vectors presenting the expressed circularly permuted proteins
 CC is generated. A target protein that can bind a biologically active
 CC circularly permuted protein can be used to affinity select the
 CC presenting display vectors. The selected display vectors can be isolated
 CC and analysed to identify the presented circularly-permuted protein. The
 CC permutins conform to the structure of a parent protein consisting of a
 CC segment derived from the carboxy portion of the parent protein, a
 CC linker or chemical bond linking the amino and carboxy terminal derived
 CC portions. Nucleotide sequences AAA35576-A35943 encode linkers used to
 CC create the permutins of the invention. The method is used to generate
 CC libraries of permutins with improved therapeutic properties compared to
 CC their parent molecules. Permutins with little or no activity may be used
 CC as antigens for producing antibodies which are used in immunology or
 CC immunotherapy as probes or intermediates used to construct other useful
 CC permutins. Permutins have improved biological and therapeutic
 CC properties compared to their two individual components due to alterations
 CC in bio-distribution or half-life.
 CC
 SQ Sequence 36 BP; 3 A; 15 C; 10 G; 8 T; 0 other;
 Query Match 58.5%; Score 15.2; DB 21; Length 36;
 Best Local Similarity 85.0%; Pred. No. 1.5e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 6 CATGCTTTGGTCCACGTA 25
 1 TGGTCATGCTTTGGTCCACGTA 25
 DB 9 CATGCTTTGGGCGCCGCGCA 28
 RESULT 10
 AAL31378/c
 ID AAL31378 standard; DNA; 50 BP.
 AC AAL31378;
 XX
 DT 24-JAN-2002 (first entry)
 DE Human SNP oligonucleotide #4586.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US35498.
 XX
 PR 28-DEC-1999; 99US-0173419.
 XX
 PR 27-DEC-2000; 2000US-0173419.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 XX
 PT

CC invention. The mahogany genes are used: (i) to produce recombinant
CC mahogany (mg) proteins (II); (ii) as a source of antisense, ribozyme or
CC triplex-forming therapeutics; (iii) as a source of diagnostic probes and
CC primers for detecting expression of mg genes or mutations; regulatory
CC defects. In this gene, or for isolation of related sequences; and
CC (iv) in (cell-based) gene therapy. (ii) are used to raise specific
CC antibodies (Ab); to identify other (extra)cellular products involved in
CC weight regulation, and to screen for agents that disrupt interaction
CC between (ii) and other macromolecules. The Ab are used to detect abnormal
CC levels (or function) of (ii) (for diagnosis, prognosis or monitoring of
CC treatment); to evaluate (ii)-expressing cells intended for cell therapy,
CC and as therapeutic mg inhibitors. Cells that express the mg gene (or
CC contain the mg polypeptide) are used to identify agents (A) that modulate
CC mg activity. (A) are potentially useful for the treatment of body weight
CC disorders, particularly obesity, cachexia or anorexia, or other
CC conditions associated with the mg gene such as hyperpigmentation,
CC hyperphagia and disorders that result in increased metabolic rate.
XX
SQ Sequence 28 BP; 13 A; 5 C; 6 G; 4 T; 0 other;

Query Match 57.7%; Score 15; DB 21; Length 28;
Best Local Similarity 78.3%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23
||||| ||||| ||||| |||||
DB 27 TGGTCATGCTTTTATCCACG 5

RESULT 13
AAK36190/C
ID AAK36190 standard; DNA; 44 BP.

XX AAK36190;
XX
XX 16-JUL-1999 (first entry)

DE Intronic location where the LTR trapping construct integrates.

XX
XX Infectious virus; recombinant viral genome; chimeric integrase;
KM mutagenesis; gene trapping; retroviral integration;
KM provirus formation; ss.

XX Unidentified.

XX MO9907389-A1.

XX 18-FEB-1999.

XX 06-AUG-1998; 98WO-US16373.

XX 08-AUG-1997; 97US-0907598.

XX (LEXI-) LEXICON GENETICS INC.

XX Burgess R, Friedrich GA, Sands AT, Zambrowicz B;

XX WPI; 1999-287449/24.

PT New infectious viruses - comprising a recombinant viral genome and
PT a chimeric integrase, used particularly for targeted gene discovery
XX
XX Disclosure; Fig 10B; 95pp; English.

XX The specification describes an infectious virus which comprises a
CC recombinant viral genome and a chimeric integrase. The chimeric
CC integrase can provide an infectious recombinant virus that is capable
CC of infecting higher eukaryotic cells and incorporates a chimeric
CC integrase activity that has been engineered to target and guide
CC viral integration to specific regions of the genome of living cells.
CC The viruses can be used in methods for the rapid identification and
CC mutagenesis, via gene trapping, of genes encoding, regulated by, or
CC adjacent to, target sequences for DNA binding proteins. They allow

CC for retroviral integration and provirus formation to occur at any
CC location within the genome. By deleting the naturally occurring
CC nonspecific DNA binding domain of the integrase, the amount of
CC random integration of viral DNA into the host genome is reduced. This
CC allows for a more efficient and high throughput analysis of target
CC sites. The present sequence represents the sequence of the intronic
CC location where the LTR trapping construct integrates.
XX

SQ Sequence 44 BP; 9 A; 14 C; 12 G; 9 T; 0 other;

Query Match 57.7%; Score 15; DB 20; Length 44;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23
||||| ||||| ||||| |||||
DB 26 TAGCCATGCTTTATCCACG 4

RESULT 14
AAL29694
ID AAL29694 standard; DNA; 50 BP.

XX AAL29694;
XX

XX 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #2902.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;

KM amyloid protein; angiotensin; apoptosis related protein; cadherin;

KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KM complement related protein; cytochrome; kinesin; cytokine; interferon;

KM interleukin; G-protein coupled receptor; thioesterase; inflammation;

KM multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

PT oncogenes and histones, useful for diagnosing and treating, e.g.

PT cancer, autoimmune diseases and infections -

XX Claim 1; Page 2217; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

CC systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukaemia), diseases of the nervous system and an infection of pathogenic
CC organisms.
XX

SQL Sequence 50 BP; 14 A; 11 C; 12 G; 13 T; 0 other;

Query Match 57.7%; Score 15; DB 22; Length 50;
Best Local Similarity 78.3%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGGTCATGCTTTGGTCCAGC 23
DB 19 TGGTCATGCTGTATCCAGC 41

RESULT 15

ABN87593/c
ID ABN87593 standard; DNA; 41 BP.

AC ABN87593;

DT 07-AUG-2002 (first entry)

DE Oligodendrocyte-myelin glucoprotein 9.68 probe 2 SEQ ID NO:9.

KW Human; oligodendrocyte-myelin glucoprotein 9.68; probe; ss;
KW nervous system dysfunction related disease.

OS Homo sapiens.

PN CN1333225-A.

PD 30-JAN-2002.

PF 07-JUL-2000; 2000CN-0117081.

PR 07-JUL-2000; 2000CN-0117081.

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

PI Mao Y, Xie Y;

DR WPI; 2002-292915/34.

PT Novel polypeptide--oligodendrocyte-myelin glucoprotein 9.68 and
PT polynucleotide for encoding the polypeptide -

PS Example 6; Page 22 (Disclosure); 34pp; Chinese.

CC The present invention describes human oligodendrocyte-myelin glucoprotein
CC 9.68 (I). Also described is a method for producing (I) using DNA
CC recombination technology. (I) can be used in the treatment of several
CC diseases, such as nervous system dysfunction related diseases. The
CC present sequence represents a probe for (I), which is used in an
CC example from the present invention.

SQL Sequence 41 BP; 5 A; 8 C; 16 G; 12 T; 0 other;

Query Match 56.9%; Score 14.8; DB 24; Length 41;
Best Local Similarity 73.1%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TGGTCATGCTTTGGTCCAGCTAC 26
DB 29 TGGACCAAGTCCAGGCCCACTTAC 4

Search completed: June 21, 2003, 22:26:21
Job time : 145.594 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 : Search time 30.875 Seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26

Sequence: 1 TGGTGCAATGCTTTGGTCCAGCTAC 26

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	17.6	67.7	47	US-09-641-638-660	Sequence 660, App
2	15.2	58.5	20	US-08-117-952-594	Sequence 594, App
3	15	57.7	28	US-09-245-041-105	Sequence 105, App
4	15	57.7	44	US-08-907-598-10	Sequence 10, Appl
5	14.8	56.9	20	US-09-851-896-84	Sequence 84, Appl
6	14.8	56.9	36	US-07-971-819A-32	Sequence 32, Appl
7	14.8	56.9	36	US-07-977-434-28	Sequence 32, Appl
8	14.8	56.9	36	US-08-475-231-32	Sequence 32, Appl
9	14.8	56.9	36	US-08-458-819-28	Sequence 28, Appl
10	14.8	56.9	36	PCR-US91-07035-28	Sequence 28, Appl
11	14.4	55.4	20	US-08-223-177A-270	Sequence 270, App
12	14.4	55.4	41	US-08-239-256-18	Sequence 18, App
13	14.4	55.4	41	5177193-20	Patent No. 5177193
14	14.2	54.6	42	US-09-286-959B-12	Sequence 12, Appl
15	14.2	54.6	42	US-08-283-857-9	Sequence 9, Appl
16	13.6	52.3	33	US-09-461-697-134	Sequence 134, App
17	13.6	52.3	38	US-08-963-946-10	Sequence 10, Appl
18	13.6	52.3	39	US-08-963-946-8	Sequence 8, Appl
19	13.6	52.3	39	US-08-964-020-12	Sequence 12, Appl
20	13.4	51.5	17	US-09-286-529-11	Sequence 11, Appl
21	13.4	51.5	30	US-09-306-998-8	Sequence 8, Appl
22	13.4	51.5	21	US-08-503-062-24	Sequence 24, Appl
23	13.4	51.5	30	PCR-US96-11495-24	Sequence 24, Appl
24	13.4	51.5	35	US-08-463-224-43	Sequence 43, Appl
25	13.4	51.5	35	US-08-463-377-43	Sequence 43, Appl
26	13.4	51.5	39	US-08-463-224-44	Sequence 44, Appl
27	13.4	51.5	39	US-08-463-377-44	Sequence 44, Appl

28	13.4	51.5	40	US-07-927-391-21	Sequence 21, Appl
29	13.2	50.8	32	US-07-987-264-18	Sequence 18, Appl
30	13.2	50.8	40	US-07-987-264-24	Sequence 24, Appl
31	13.2	50.8	43	US-09-489-979-2	Sequence 2, Appl
32	13.2	50.8	49	US-09-302-620B-76	Sequence 76, Appl
33	13	50.0	28	US-09-609-816-21	Sequence 21, Appl
34	13	50.0	29	US-08-295-676A-15	Sequence 15, Appl
35	13	50.0	29	US-08-948-591-15	Sequence 15, Appl
36	13	50.0	32	US-08-362-525-5	Sequence 5, Appl
37	13	50.0	47	US-09-641-638-1157	Sequence 1157, Ap
38	13	50.0	50	5464943-3	Patent No. 5464943
39	12.8	49.2	18	US-09-071-433-57	Sequence 57, Appl
40	12.8	49.2	25	US-08-348-891A-16	Sequence 16, Appl
41	12.8	49.2	25	US-08-905-817-16	Sequence 16, Appl
42	12.8	49.2	29	US-08-471-058-4	Sequence 4, Appl
43	12.8	49.2	29	US-08-471-057-4	Sequence 4, Appl
44	12.8	49.2	34	US-08-178-476A-17	Sequence 17, Appl
45	12.8	49.2	34	US-08-257-073-136	Sequence 136, App

ALIGNMENTS

```
RESULT 1
US-09-641-638-660
; Sequence 660, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bouquelere, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GENSET, 051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 660
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-500-258 : polymorphic base G or T
; NAME/KEY: misc-feature
; LOCATION: 1
; OTHER INFORMATION: n=a, g, c or t
US-09-641-638-660

Query Match
Best Local Similarity 67.7%; Score 17.6; DB 4; Length 47;
Matches 20; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 TGGTGCAATGCTTTGGTCCAGCTAC 26
      |||||  |||  |||||
Db      13 TGGTGCAATGCTTTGGTCCAGCTAC 38

RESULT 2
US-08-117-952-594/c
; Sequence 594, Application US/08117952
; Patent No. 5851760
```

GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 594:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Oligonucleotide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-117-952-594

Query Match 58.5%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGCTTTGGTCCGACTAC 26
DB 20 ATCCCTTGCTGCCAGCTAC 1

RESULT 3
US-09-245-041-105/C
Sequence 105, Application US/09245041
GENERAL INFORMATION:
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REFERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/093,630
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/104,978
NUMBER OF SEQ ID NOS: 131
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 105
LENGTH: 281
TYPE: DNA

ORGANISM: Artificial sequence
US-09-245-041-105

Query Match 57.7%; Score 15; DB 4; Length 28;
Best Local Similarity 78.3%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGTGCATGCTTTGTGCCACG 23
DB 27 TGTTCATCCTTTATATCCACG 5

RESULT 4
US-08-907-598-10/C
Sequence 10, Application US/08907598
Patent No. 6139833
GENERAL INFORMATION:
APPLICANT: Burgess, Rob
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur
TITLE OF INVENTION: TARGETED GENE DISCOVERY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,598
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8535-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-4935
TELEFAX: (650) 493-5556
TELEX: 66141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-907-598-10

Query Match 57.7%; Score 15; DB 3; Length 44;
Best Local Similarity 78.3%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGTGCATGCTTTGTGCCACG 23
DB 26 TAGCCATGCCCTTAGTCCACG 4

RESULT 5
US-09-851-896-84
Sequence 84, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freiler

APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
FILE REFERENCE: RUS-0220
CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 84
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-851-896-84

Query Match 56.9%; Score 14.8; DB 4; Length 20;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 CATGCTTTGGTCCGAC 23
||| ||||| ||||| |||
1 CATTTCTTAGTCCGAC 18

Db

RESULT 6
US-07-971-819A-32
Sequence 32, Application US/07971819A
Patent No. 5420029
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Purified Thermostable Nucleic Acid
TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,819A
FILING DATE: 19930203
CLASSIFICATION: A43
ATTORNEY/AGENT INFORMATION:
NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid
US-07-971-819A-32

Query Match 56.9%; Score 14.8; DB 1; Length 36;
Best Local Similarity 73.1%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TGGTGATGCTCTTGTGTCACGCTAC 26

Db 2 TGAACATGCTTTGTGTCACGCTAC 27
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RESULT 7
US-07-977-434-28
Sequence 28, Application US/07977434
Patent No. 546591
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Adrison, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: Wordperfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
FILING DATE:
CLASSIFICATION: A43
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luann Casert
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 546591 8753
TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA primer FL64
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-07-977-434-28

Query Match 56.9%; Score 14.8; DB 1; Length 36;
Best Local Similarity 73.1%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGTAC 26
11 1111111111 11 111
DB 2 TGAGCATGCTTTGTCCACGGTTAC 27

RESULT 8

US-08-475-231-32
Sequence 32, Application US/08475231
Patent No. 5624833
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Lawyer, Frances C.
APPLICANT: Stoffel, Susanne
TITLE OF INVENTION: Purified Thermostable Nucleic Acid
TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,231
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,819
FILING DATE: 03-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid
US-08-475-231-32

Query Match 56.9%; Score 14.8; DB 1; Length 36;
Best Local Similarity 73.1%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TGGTGCATGCTTTGGTCCACGTAC 26

DB 11 1111111111 11 111
2 TGAGCATGCTTTGTCCACGGTTAC 27

RESULT 9

US-08-458-819-28
Sequence 28, Application US/08458819
Patent No. 5795762
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,819
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,434
FILING DATE: 23-FEB-1993
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luann Cseer
REGISTRATION NUMBER: 31,822


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REFERENCE/DOCKET NUMBER: Case No. 5795762 87/53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA primer FL64
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-458-819-28

Query Match      56.9%; Score 14.8; DB 1; Length 36;
Best Local Similarity 73.1%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1  TGGTGCATGCTTGTGTCACGCTAC 26
        14  ||||| 11111111 11 11111
Db      2  TGAAGCATGCTCTTGTCTACCGCTTAC 27

RESULT 10
PCT-US91-07035-28
Sequence 28, Application PC/TUS9107035
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation
STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641

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1  FILING DATE: 21-DEC-1990
2  PRIOR APPLICATION DATA:
3  APPLICATION NUMBER: US 585,471
4  FILING DATE: 20-SEP-1990
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: US 455,611
7  FILING DATE: 22-DEC-1989
8  PRIOR APPLICATION DATA:
9  APPLICATION NUMBER: US 609,157
10 FILING DATE: 02-NOV-1990
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 557,517
13 FILING DATE: 24-JUL-1990
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Sias Ph.D, Stacey R.
16 REGISTRATION NUMBER: 32,630
17 REFERENCE/DOCKET NUMBER: Case No. 2580
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 415-420-3300
20 INFORMATION FOR SEQ ID NO: 28:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 36 nucleotides
23 TYPE: NUCLEIC ACID
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: DNA primer FL64
27 HYPOTHETICAL: NO
28 ANTI-SENSE: NO
29 PCT-US91-07035-28
30
31 Query Match 56.9%; Score 14.8; DB 5; Length 36;
32 Best Local Similarity 73.1%; Pred. No. 2.5e+02;
33 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
34
35 QY 1 TGGTGCATGCTTTGGTCCAGCTAC 26
36 || ||||| ||||| || |||||
37 DB 2 TGAGCATGCTTTGTCCACGGTTAC 27
38
39 RESULT 11
40 US-08-222-177A-270
41 ; Sequence 270 Application US/08222177A
42 ; Patent No. 5582979
43 ; GENERAL INFORMATION:
44 APPLICANT: Weber, James L.
45 TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
46 TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
47 NUMBER OF SEQUENCES: 460
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Demilt Ross & Stevens, S.C.
50 STREET: 8000 Excelsior Drive, Suite 401
51 CITY: Madison
52 STATE: Wisconsin
53 COUNTRY: USA
54 ZIP: 53717-1914
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: PatentIn Release #1.0, Version #1.25
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/08/222,177A
62 FILING DATE:
63 CLASSIFICATION: 435
64 PRIOR APPLICATION DATA:
65 APPLICATION NUMBER: US 07/341,562
66 FILING DATE: 21-APR-1989
67 ATTORNEY/AGENT INFORMATION:
68 NAME: Sara, Charles S.
69 REGISTRATION NUMBER: 30,492
70 REFERENCE/DOCKET NUMBER: 09865,601
71 TELECOMMUNICATION INFORMATION:
72 TELEPHONE: (608) 831-2100
73

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1 TELEFAX: (608) 831-2106
2
3 TELEX:
4
5 INFORMATION FOR SEQ ID NO: 270
6
7 SEQUENCE CHARACTERISTICS:
8
9 LENGTH: 20 base pairs
10
11 TYPE: nucleic acid
12
13 STRANDEDNESS: double
14
15 TOPOLOGY: linear
16
17 MOLECULE TYPE: DNA (genomic)
18
19 IMMEDIATE SOURCE:
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21 CLONE: mcd78p2
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Query Match	55.48;	Score 14.4;	DB 1;	Length 20;
Best Local Similarity	93.88;	Pred. No. 3.6e+02;		
Matches 15; Conservative	0;	Mismatches 1;	Indels	

Oy	8	TGTCCTTGSTCCAGC	23
	1		
	4	TGCTATGSTCCAGC	19
Db			

RESULT 12
US-08-239

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US-08-239-256-18
: Sequence 18: Application US/08239256
: Patent No. 5585345
:
: GENERAL INFORMATION:
: APPLICANT: BOIME, IRVING
: APPLICANT: MATZUR, MARTIN M.
: APPLICANT: KEENE, JEFFREY L.
: TITLE OF INVENTION: CTP EXTENDED FORM OF LH
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Ave. N.W.
: CITY: Washington, D.C.
: COUNTRY: USA
: ZIP: 20006-1812
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/239,256
: FILING DATE: 06-MAY-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 29500-20030.12
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
:
: TELEX: 90-4030
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 41 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: Linear
:
: US-08-239-256-18

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Query Match	55.48;	Score 14.4;	DB 1;	Length 41;
Best Local Similarity	75.08;	Pred. No. 4e+02;		
Matches 18; Conservative	0;	Mismatches 6;	Indels	

QY		3 GTGCATGCTTTGGTCCACGTAC	26
Db		7 GTGCGAGCCTGGGCCACGTAC	30

RESÜLT 13

5177193-20
Patent No. 5177193
APPLICANT: BOJME, IRVING; MATZUK, MARTIN M.
TITLE OF INVENTION: MODIFIED FORMS OF REPRODUCTIVE HORMONES
NUMBER OF SEQUENCES: 26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/532,254
FILING DATE: 01-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 313,646
FILING DATE: 21-FEB-1989
SEQ ID NO.:20
LENGTH: 41
5177193-20

Query Match	55.4%	Score 14.4	DB 6	Length 41
Best Local Similarity	75.0%	Pred. No. 4e+02		
Matches 18	Conservative 0	Mismatches 6	Indels 0	Gaps 0

QY	3	GTGCATGCTTTGGTCCAGCTAC	26
Db	7	GTGCGAGGCGCTGGGCCAGCTAC	30

RESULT 14

```

Sequence 12, Application us/09286959B
Patent No. 6300131
GENERAL INFORMATION:
APPLICANT: Johns Hopkins University
APPLICANT: Gelder, Carol W.
APPLICANT: Le, SiYuan
TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
FILE REFERENCE: 07265/157001
CURRENT APPLICATION NUMBER: US/09/286,959B
CURRENT FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: 60/080,763
PRIOR FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTED for Windows Version 4.0
SEO ID NO 12
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-286-959B-12

```

Query Match	54.6%	Score 14.2	DB 4	Length 20
Best Local Similarity	84.2%	Pred. No. 4.4e+02		
Matches 16	Conservative 0	Mismatches 3	Indels 0	Gaps 0

Qy	8	TGTC	TTGG	TCCAG	CTAC	26
Db	2	TGCT	TGAG	TCCAG	CTAC	20

RESULT 15

US-08-283-857-9/C
Sequence 9, Application US/08283857
Patent No. 5792742
GENERAL INFORMATION:
APPLICANT: GOLD, Leslie I.
APPLICANT: ROSFAGNO, Agueda A.
APPLICANT: BARON, Martin
APPLICANT: CAMPBELL, Iain D.
APPLICANT: WILLIAMS, Michael, J.
TITLE OF INVENTION: FIBRONECTIN FIBRIN-BINDING PEPTIDES, DNA
TITLE OF INVENTION: CODING THEREOF AND USERS THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROADY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300

```

: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/283,857
: FILING DATE: 01-AUG-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/714,134
: FILING DATE: 14-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: GOLD=1A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-628-5197
: TELEFAX: 202-737-3528
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 42 nucleotides
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: US-08-283-857-9

```

```

Query Match      54.6%; Score 14.2; DB 1; Length 42;
Best Local Similarity 84.2%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      6 CATGCTTTGGTCCAGCT 24
        ||| ||||| ||| |||
Db      26 CATCTCTTTGTCCAGCT 8

```

Search completed: June 22, 2003, 00:01:31
 Job time : 32.875 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 76.7812 Seconds
(without alignments)
496.907 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26

Sequence: 1 TGGTCATGCTTTGTCACAGCTAC 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published.Applications_NA.*
2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	9	US-09-964-667-10
2	26	100.0	26	10	US-09-964-666-10
3	26	100.0	26	10	US-09-964-666-10
4	21	80.8	39	9	US-10-198-069-46
5	15	57.7	28	10	US-09-893-238-105
6	14.8	56.9	25	9	US-10-098-263B-127897
7	14.6	56.2	23	9	US-09-860-738C-35
8	14.6	56.2	23	9	US-09-860-738C-38
9	14.6	56.2	23	9	US-09-860-738C-48
10	14.6	56.2	23	9	US-09-860-738C-53
11	14.6	56.2	23	9	US-09-860-738C-55
12	14.6	56.2	23	9	US-09-860-738C-55
13	14.6	56.2	23	9	US-09-860-738C-74
14	14.6	56.2	39	9	US-10-198-069-45
15	14.6	56.2	41	9	US-09-860-738C-36
16	14.6	56.2	41	9	US-09-860-738C-54
17	14.2	54.6	25	9	US-10-098-263B-5917
18	14	53.8	25	9	US-10-098-263B-104291
19	14	53.8	31	10	US-09-801-274-450

20	14	53.8	31	10	US-09-801-274-1391	Sequence 1391, Ap
21	14	53.8	37	9	US-10-001-876-109	Sequence 109, App
22	13.8	53.1	42	9	US-09-733-692A-30	Sequence 30, Appl
23	13.6	52.3	25	9	US-10-098-263B-23537	Sequence 23537, A
24	13.6	52.3	25	9	US-10-098-263B-130235	Sequence 130235,
25	13.6	52.3	31	10	US-09-801-274-1127	Sequence 1127, Ap
26	13.6	52.3	33	10	US-09-922-261-134	Sequence 134, App
27	13.4	51.5	17	10	US-09-877-156-11	Sequence 11, Appl
28	13.4	51.5	21	9	US-09-951-402-8	Sequence 8, Appl
29	13.4	51.5	21	10	US-09-951-401-8	Sequence 8, Appl
30	13.4	51.5	21	10	US-09-922-101-8	Sequence 8, Appl
31	13.4	51.5	25	9	US-10-098-263B-1457	Sequence 1457, Ap
32	13.4	51.5	25	9	US-10-098-263B-105579	Sequence 105579,
33	13.4	51.5	25	9	US-10-098-263B-121069	Sequence 121069
34	13.4	51.5	31	9	US-09-912-263-435	Sequence 435, App
35	13.4	51.5	32	10	US-09-795-006A-4	Sequence 4, Appl
36	13.4	51.5	37	9	US-09-780-164-1792	Sequence 1792, Ap
37	13.4	51.5	42	10	US-09-795-006A-13	Sequence 13, Appl
38	13.2	50.8	22	9	US-10-198-069-39	Sequence 39, Appl
39	13.2	50.8	25	9	US-10-098-263B-36336	Sequence 36336, A
40	13.2	50.8	25	9	US-10-098-263B-59077	Sequence 59077, A
41	13.2	50.8	25	9	US-10-098-263B-76416	Sequence 76416, A
42	13.2	50.8	25	9	US-10-098-263B-111162	Sequence 111162,
43	13.2	50.8	25	9	US-10-098-263B-116373	Sequence 116373,
44	13.2	50.8	25	9	US-10-098-263B-127898	Sequence 127898,
45	13.2	50.8	28	9	US-10-198-069-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-964-667-10
Sequence 10, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Mands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-667-10

Query Match 100.0%; Score 26; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCACGCTAC 26

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 2

US-09-964-666-10

Sequence 10, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-666-10

Query Match 100.0%; Score 26; DB 10; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCACGCTAC 26

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 3

US-09-964-412-10

Sequence 10, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-964-412-10

Query Match 100.0%; Score 26; DB 10; Length 26;

Best Local Similarity 100.0%; Pred. No. 0.0055;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCACGCTAC 26

DB 1 TGGTGCATGCTTTGGTCCACGCTAC 26

RESULT 4

US-10-198-069-46/c

Sequence 46, Application US/10198069

Publication No. US20030096756A1

GENERAL INFORMATION:

APPLICANT: AVERBACK, PAUL

TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER

CONDITIONS, REQUIRING THE REMOVAL OR DESTRUCTION OF

FILE REFERENCE: 59003.000009

CURRENT APPLICATION NUMBER: US/10/198,069

CURRENT FILING DATE: 2002-07-19

PRIOR APPLICATION NUMBER: 60/306,161

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/306,150

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 46

LENGTH: 39

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-198-069-46

Query Match 80.8%; Score 21; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CATGCTTGTCCTCCAGCTAC 26
|||||
DB 39 CATGCTTGTCCTCCAGCTAC 19

RESULT 5

US-09-893-238-105/c
; Sequence 105, Application US/09893238
; Patent No. US20020150973A1
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 105
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-893-238-105

Query Match 57.7%; Score 15; DB 10; Length 28;
Best Local Similarity 78.3%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTCTTTGGTCCAGC 23
|||||
DB 27 TGGTCATGCTCTTTATCCAGC 5

RESULT 6

US-10-098-263B-127897
; Sequence 127897, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 127897
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-127897

Query Match 56.9%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GTGCATGCTTTGGTCC 20
|||||
DB 4 GTGCAGTCTTGGTCC 21

RESULT 7

US-09-860-738C-35
; Sequence 35, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Langmore, John
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-35

Query Match 56.2%; Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0%; Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTGCATGCTTTGGTCCAG 22
|||||
DB 2 GTGCATGCTATGTCGCGAG 22

RESULT 8

US-09-860-738C-38
; Sequence 38, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Primer
US-09-860-738C-38

Query Match 56.2%; Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0%; Pred. No. 8.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTGCATGCTTTGGTCCAG 22
|||||
DB 2 GTGCATGCTATGTCGCGAG 22

RESULT 9

US-09-860-738C-48
; Sequence 48, Application US/09860738C
; Publication No. US20030040620A1
; GENERAL INFORMATION:
; APPLICANT: Langmore, John
; APPLICANT: Makarov, Vladimir
; TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplificati
; FILE REFERENCE: UMIC:047US0/10103482
; CURRENT APPLICATION NUMBER: US/09/860,738C
; CURRENT FILING DATE: 2001-05-18

NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 23
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Primer
US-09-860-738C-48

Query Match 56.2% Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0% Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGCATGCTTGTGTCGCGAG 22
||||||| | | | | | | |
Db 2 GGTGCATGCTGTATCGTCGCGAG 22

RESULT 10
US-09-860-738C-50
Sequence 50, Application US/09860738C
Publication No. US20030040620A1
GENERAL INFORMATION:
APPLICANT: Langmore, John
APPLICANT: Makarov, Vladimir
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
FILE REFERENCE: UMIC:047US0/10103482
CURRENT APPLICATION NUMBER: US/09/860,738C
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 23
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Primer
US-09-860-738C-50

Query Match 56.2% Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0% Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGCATGCTTGTGTCGCGAG 22
||||||| | | | | | | |
Db 2 GGTGCATGCTGTATCGTCGCGAG 22

RESULT 11
US-09-860-738C-53
Sequence 53, Application US/09860738C
Publication No. US20030040620A1
GENERAL INFORMATION:
APPLICANT: Langmore, John
APPLICANT: Makarov, Vladimir
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
FILE REFERENCE: UMIC:047US0/10103482
CURRENT APPLICATION NUMBER: US/09/860,738C
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 53
LENGTH: 23
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Primer
US-09-860-738C-53

Query Match 56.2% Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0% Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGCATGCTTGTGTCGCGAG 22
||||||| | | | | | | |
Db 2 GGTGCATGCTGTATCGTCGCGAG 22

RESULT 12
US-09-860-738C-55
Sequence 55, Application US/09860738C
Publication No. US20030040620A1
GENERAL INFORMATION:
APPLICANT: Langmore, John
APPLICANT: Makarov, Vladimir
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
FILE REFERENCE: UMIC:047US0/10103482
CURRENT APPLICATION NUMBER: US/09/860,738C
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 23
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Primer
US-09-860-738C-55

Query Match 56.2% Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0% Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGCATGCTTGTGTCGCGAG 22
||||||| | | | | | | |
Db 2 GGTGCATGCTGTATCGTCGCGAG 22

RESULT 13
US-09-860-738C-74
Sequence 74, Application US/09860738C
Publication No. US20030040620A1
GENERAL INFORMATION:
APPLICANT: Langmore, John
APPLICANT: Makarov, Vladimir
TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
FILE REFERENCE: UMIC:047US0/10103482
CURRENT APPLICATION NUMBER: US/09/860,738C
CURRENT FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.1
SEQ ID NO 74
LENGTH: 23
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Primer
US-09-860-738C-74

Query Match 56.2% Score 14.6; DB 9; Length 23;
Best Local Similarity 81.0% Pred. No. 1.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGTGCATGCTTGTGTCGCGAG 22
||||||| | | | | | | |
Db 2 GGTGCATGCTGTATCGTCGCGAG 22

RESULT 14
US-10-198-069-45/C
Sequence 45, Application US/10198069
Publication No. US20030096756A1
GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER


```

: TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
: TITLE OF INVENTION: CELLS
: FILE REFERENCE: 59003.000009
: CURRENT APPLICATION NUMBER: US/10/198,069
: CURRENT FILING DATE: 2002-07-19
: PRIOR APPLICATION NUMBER: 60/306,161
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/306,150
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/331,477
: PRIOR FILING DATE: 2001-11-16
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 45
: LENGTH: 39
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: US-10-198-069-45

```

```

Query Match      56.2%; Score 14.6; DB 9; Length 39;
Best Local Similarity 81.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY      6 CATGCTTTGGTCCGACTAC 26
      ||| || | |||||
Db      39 CATGCTGTATCCGACTAC 19

```

```

RESULT 15
US-09-860-738C-36/c
: Sequence 36, Application US/09860738C
: Publication No. US20030040620A1
: GENERAL INFORMATION:
: APPLICANT: Langmore, John
: APPLICANT: Makarov, Vladimir
: TITLE OF INVENTION: Method of Producing a DNA Library Using Positional Amplification
: FILE REFERENCE: UMC:047US0/10103482
: CURRENT APPLICATION NUMBER: US/09/860,738C
: CURRENT FILING DATE: 2001-05-18
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO: 36
: LENGTH: 41
: TYPE: DNA
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Primer
: US-09-860-738C-36

```

```

Query Match      56.2%; Score 14.6; DB 9; Length 41;
Best Local Similarity 81.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY      2 GGTGCATGCTTTGGTCCAG 22
      ||||| | | |||
Db      40 GGTGCATGCTATCGTCCAG 20

```

Search completed: June 22, 2003, 03:18:16
Job time : 78,7812 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 1123.08 Seconds
(without alignments)
374.936 Million cell updates/sec

Title: US-09-964-666-10

Perfect score: 26
Sequence: 1 TCGTCATGCTTGTGTCACACTAC 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_estl:*
10: gb_est2:*
11: gb_estc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gse:*
18: em_gse_hum:*
19: em_gse_inv:*
20: em_gse_pln:*
21: em_gse_vrt:*
22: em_gse_fun:*
23: em_gse_mam:*
24: em_gse_mus:*
25: em_gse_other:*
26: em_gse_pro:*
27: em_gse_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.2	73.8	42	14	H47110 yp77e03.s1
C 2	18	69.2	40	14	N95034 zb32b05.s1
C 3	18	69.2	45	14	T92229 ye17f11.r1
4	17	65.4	48	14	N79917 yz86a06.r1
5	16.8	64.6	33	14	H85333 ys90e04.r1
C 6	16.6	63.8	34	17	AZ393855 IM0157D07

C 7	16.6	63.8	48	17	AZ496155	AZ496155 IM0332K15
C 8	16.2	62.3	32	14	T92842	T92842 ye27a08.r1
C 9	16.2	62.3	32	14	T92862	T92862 ye27a08.r1
C 10	15.6	60.0	24	17	AZ831249	AZ831249 2M0110G21
C 11	15.2	58.5	28	14	T90404	T90404 ye16c02.r1
C 12	15.2	58.5	28	14	T94189	T94189 ye29h12.r1
C 13	15.2	58.5	33	14	N67043	N67043 za50e12.s1
C 14	15	57.7	38	17	AZ489704	AZ489704 1M0238E19
C 15	15	57.7	41	17	AZ489704	AZ489704 1M0322L14
C 16	15	57.7	42	9	AA868654	AA868654 ak49i09.s
C 17	15	57.7	43	14	H09843	H09843 ym01d05.r1
C 18	15	57.7	43	14	R61212	R61212 yho0e10.r1
C 19	15	57.7	46	17	AZ471093	AZ471093 1M0285F01
C 20	14.8	56.9	34	14	N63645	N63645 za16f12.s1
C 21	14.8	56.9	50	9	AU102380	AU102380 AU102380
C 22	14.4	55.4	31	17	AZ393593	AZ393593 1M0156A14
C 23	14.2	54.6	50	9	AU102523	AU102523 AU102523
C 24	14.2	54.6	50	17	AZ809862	AZ809862 2M0074K06
C 25	14	53.8	24	17	AZ822910	AZ822910 2M0096N02
C 26	14	53.8	50	14	H60434	H60434 yf42c06.s1
C 27	13.8	53.1	25	17	AZ635949	AZ635949 1M0493C08
C 28	13.8	53.1	47	17	AL754182	AL754182 Arabidops
C 29	13.8	53.1	49	9	AA458130	AA458130 vg46a07.r
C 30	13.6	52.3	28	14	H70161	H70161 yso1h11.r1
C 31	13.6	52.3	42	14	R84748	R84748 yf68h09.r1
C 32	13.6	52.3	43	14	H69549	H69549 yf99e04.s1
C 33	13.6	52.3	47	14	R55441	R55441 yf79d08.r1
C 34	13.4	51.5	28	17	AZ361627	AZ361627 1M0106H17
C 35	13.4	51.5	31	17	AZ659725	AZ659725 1M0537O13
C 36	13.4	51.5	32	14	H46868	H46868 yoi19b04.r1
C 37	13.4	51.5	38	13	B1112512	B1112512 602900A52
C 38	13.4	51.5	50	9	AU102375	AU102375 AU102375
C 39	13.4	51.5	50	9	AU102386	AU102386 AU102386
C 40	13.4	51.5	50	14	N26705	N26705 yx61b10.s1
C 41	13.2	50.8	33	13	BM392790	BM392790 50071-2-1
C 42	13.2	50.8	33	13	BM394082	BM394082 50072-2-1
C 43	13.2	50.8	36	14	R44635	R44635 yf28a09.s1
C 44	13.2	50.8	50	9	AU102384	AU102384 AU102384
C 45	13	50.0	24	17	TA57D02P	TA57D02P T. brucei

ALIGNMENTS

RESULT 1
LOCUS H47110/c 42 bp mRNA linear EST 16-AUG-1995
DEFINITION yp77e03.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:193468 3' similar to gb:Z13009_rnal EPITHELIAL-CADHERIN
PRECURSOR (HUMAN); mRNA sequence.

ACCESSION H47110
VERSION H47110.1 GI:923162

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 42)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviski,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project

Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu
Insert Size: 704

High quality sequence starts: 1
High quality sequence stops: 1

/db_xref="taxon:9606"
/clone="IMAGE:118029"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="50LR cells (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI
; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; uni-ZAP XR
vector; -5' adaptor sequence: 5' GATTTCGCACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT
ORIGIN
13 a 12 c 11 g 9 t

Query Match
Best Local Similarity 69.2%; Score 18; DB 14; Length 45;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCAGCTAC 26
111 111 111 111 111 111
30 TGGCACATGCGCTATGCTCTACTAC 5

RESULT 4 48 bp mRNA linear EST 02-APR-1996
N79917 yz86a06.r1 Soares multiple_sclerosis_2NBHMP Homo sapiens cDNA
LOCUS clone IMAGE:289906 5' similar to gb|U87911|HUMANES7 Human
DEFINITION carcinoma cell-derived Alu RNA transcript, (rRNA); gb:X34150.rna1
IMMUNOGLOBULIN ALPHA FC RECEPTOR PRECURSOR (HUMAN); contains element
MER22 repetitive element; mRNA sequence.
N79917
EST. N79917.1 GI:1242618

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 48)
Miller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: reverse ET
High quality sequence stop: 1.
Location/Qualifiers
1. 48
/organism="Homo sapiens"
/db_xref="GDB:3905746"
/db_xref="taxon:9606"
/clone="IMAGE:289906"
/clone_lib="Soares_multiple_sclerosis_2NBHMP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pTZ19 (Pharmacia) with a modified
polylinker V-type phagemid; Site: 1: Not I; Site: 2: Eco RI
primer [5'
TGTTCACATCTGAAGTGGAGCGCCGCAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was provided by Dr. Kevin
G. Becker (MIND/NIH). "

BASE COUNT
ORIGIN
7 a 7 c 18 g 15 t 1 others

Query Match
Best Local Similarity 65.4%; Score 17; DB 14; Length 48;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TGGTGCATGCTTTGGTCCAGCTAC 26
111 111 111 111 111 111
15 TGGTGTGCTCTGTATNCCAGCTAC 40

RESULT 5 33 bp mRNA linear EST 14-NOV-1995
H85333 y90e04.r1 Soares retina N2B5HR Homo sapiens cDNA clone
LOCUS IMAGE:222078 5' similar to gb:Y00281 RIBOPHORIN I PRECURSOR (HUMAN
DEFINITION); mRNA sequence.
H85333
VERSION H85333.1 GI:1064274
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 33)
Miller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maita, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2596 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1. 33
/organism="Homo sapiens"
/db_xref="GDB:3850839"
/db_xref="taxon:9606"
/clone="IMAGE:222078"
/clone_lib="Soares retina N2B5HR"
/sex="male"
/tissue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: eye; Vector: pTZ19 (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site: 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCCGCAATTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pTZ19 vector
(Pharmacia). The retinas were obtained from a 55 year old

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 12 a 21 c 8 g 7 t

Query Match 63.8%; Score 16.6; DB 17; Length 48;
Best Local Similarity 82.6%; Pred. No. 4.6e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCAGC 23
||||| | ||| | ||| |
Db 23 TGTGTCAGCCTTATCCAGC 1

RESULT 8
T92842/c
LOCUS
DEFINITION T92842 32 bp mRNA linear EST 22-MAR-1995
ye27a08.r1 Stratagene Lung (#937210) Homo sapiens cDNA clone
IMAGE:118934.5' similar to gb:213009_rna1 EPITHELIAL-CADHERIN
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION T92842 GI:724755
VERSION T92842.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
1 (bases 1 to 32)

Chissoe,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE JOURNAL MEDLINE

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

Insert Size: 451

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality

Insert length: 451 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
/db_xref="GDB:487223"
/db_xref="taxon:9606"
/clone="IMAGE:118934"
/clone_lib="Stratagene Lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: Lung; Vector: pBluescript SK-; Site:1: ECORI
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

BASE COUNT 9 a 10 c 8 g 5 t

ORIGIN

Query Match 62.3%; Score 16.2; DB 14; Length 32;

Best Local Similarity 85.7%; Pred. No. 6.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCAGCTAC 26
||||| | ||| | ||| |
Db 32 CATGCTATGCTCTAGCTAC 12

RESULT 9
T92862/c
LOCUS
DEFINITION T92862 32 bp mRNA linear EST 22-MAR-1995
ye27e08.r1 Stratagene Lung (#937210) Homo sapiens cDNA clone
IMAGE:118982.5' similar to gb:213009_rna1 EPITHELIAL-CADHERIN
PRECUSOR (HUMAN);, mRNA sequence.

ACCESSION T92862 GI:724775
VERSION T92862
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
1 (bases 1 to 32)

Chissoe,S., Dietrich,N., Dubuque,T., Favellio,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevasakis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478

TITLE JOURNAL MEDLINE

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

Insert Size: 565

High quality sequence starts: 1 High quality sequence stops: 1

Source: IMAGE Consortium, LNL This clone is available royalty-free
through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality

Insert length: 565 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 1.

Location/Qualifiers

FEATURES

source

/organism="Homo sapiens"
/db_xref="GDB:487271"
/db_xref="taxon:9606"
/clone="IMAGE:118982"
/clone_lib="Stratagene Lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: Lung; Vector: pBluescript SK-; Site:1: ECORI
; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' "

BASE COUNT 9 a 10 c 8 g 5 t

ORIGIN

Query Match 62.3%; Score 16.2; DB 14; Length 32;
Best Local Similarity 85.7%; Pred. No. 6.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCAGCTAC 26
||||| | ||| | ||| |
Db 32 CATGCTATGCTCTAGCTAC 12

RESULT 10

A2831249/c
 LOCUS A2831249 24 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0110621R Mouse 10kb plasmid UUGC1M library mus musculus genomic clone UUGC2M0110621 R, DNA sequence.
 ACCESSION A2831249
 VERSION A2831249.1 GI:13001157
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 24)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10Kb Plasmid Inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH
 RM. 308, Biomedical Polymers, Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 TEL: 801 585 5606
 FAX: 801 585 7177
 EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0110 row: 6 column: 21
 SEQ PRIMER: CACACAGAACAGCTATGACC
 CLASS: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0110621"
 /clone_lib="Mouse 10Kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (911473211419b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 9 a 6 c 5 g 4 t
 Query Match 60.0%; Score 15.6; DB 17; Length 24;
 Best Local Similarity 81.8%; Pred. No. 1e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TGTGTCATGCTTTGTCGCCAG 22
 ||||| ||||| ||||| |||||
 DB 22 TGTGTCATGCTTTATTCACG 1

RESULT 11
 .

T90404/c
 LOCUS T90404 28 bp mRNA linear EST 20-MAR-1995
 DEFINITION yelc02.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:117890 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION T90404
 VERSION T90404.1 GI:718917
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 28)
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chaplin, B., Chisoe, S., Dietrich, N., Dubucq, T., Favello, A., Gish, N., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R., and Marra, M.
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 CONTACT: Wilson RK
 WASHINGTON UNIVERSITY SCHOOL OF MEDICINE
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 TEL: 314 286 1800
 FAX: 314 286 1810
 EMAIL: estewatson.wustl.edu
 INSERT SIZE: 320
 High quality sequence starts: 1 High quality sequence stops: 1
 SOURCE: IMAGE Consortium, LUNL This clone is available royalty-free through LUNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality
 INSERT LENGTH: 320 Std Error: 0.00
 SEQ PRIMER: M13Rpl
 High quality sequence stop: 1.
 Location/Qualifiers
 1..28
 /organism="Homo sapiens"
 /db_xref="GDB:486179"
 /db_xref="taxon:9606"
 /clone="IMAGE:117890"
 /clone_lib="Stratagene lung (#937210)"
 /sex="male"
 /dev_stage="72 years"
 /lab_host="SOLR cells (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT
 ORIGIN
 8 a 9 c 6 g 5 t
 Query Match 58.5%; Score 15.2; DB 14; Length 28;
 Best Local Similarity 85.0%; Pred. No. 1.6e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 ATGCTTTGGTCCAGCTAC 26
 ||| ||||| ||||| |||||
 DB 28 ATGCTATGCTCTAGCTAC 9
 RESULT 12
 T94189/c 28 bp mRNA linear EST 24-MAR-1995
 LOCUS T94189
 DEFINITION yezh12.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119207 5' similar to gb:M73700 LACTOTRANSFERRIN PRECURSOR (HUMAN);, mRNA sequence.
 ACCESSION T94189
 VERSION T94189.1 GI:727677
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 28)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chapell, B., Chissole, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, B., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

JOURNAL MEDLINE
97044478

COMMENT
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 348
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality
Insert Length: 348 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1..28
/organism="Homo sapiens"
/db_xref="GDB:487496"
/db_xref="taxon:9606"
/clone_image="IMAGE:119207"
/clone_lib="Stratagene lung (#937210)"
/sex="male"
/dev_stage="72 years"
/lab_host="SOE cells (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT
8 a 9 c 6 g 5 t

ORIGIN

Query Match 58.5%; Score 15.2; DB 14; Length 28;
Best Local Similarity 85.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ATGCTTTGGTCCACCTAC 26
|||||
1 ATGCTTTGGTCCACCTAC 9

Db 28 ATGCTTTGGTCCACCTAC 9

RESULT 13
N67043 33 bp mRNA linear EST 08-MAR-1996
LOCUS 245612.s1 Soares fetal liver spleen INFLS Homo sapiens CDNA clone
DEFINITION IMAGE:296014 3' similar to gb:K02067 H.sapiens mRNA for 7SL RNA
pseudogene (HUMAN); mRNA sequence.
ACCESSION N67043
VERSION N67043.1 GI:1219168
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 33)
Hillier, L., Clark, N., Dubuque, T., Elliston, G., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project

JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.
Location/Qualifiers
1..33
/organism="Homo sapiens"
/db_xref="GDB:1240935"
/db_xref="taxon:9606"
/clone_image="IMAGE:296014"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site: 1: Pac I; Site: 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer (5' AACGTGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'). Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
5 a 9 c 11 g 7 t 1 others

ORIGIN

Query Match 58.5%; Score 15.2; DB 14; Length 33;
Best Local Similarity 81.0%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CATGCTTTGGTCCACCTAC 26
|||||
1 CATGCTTTGGTCCACCTAC 21

Db 1 CATGCTTTGGTCCACCTAC 21

RESULT 14
AZ438336 38 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0228E19F Mouse 10kb plasmid UGCLM library Mus musculus genomic
DEFINITION clone UGCLM0228E19 F, DNA sequence.
ACCESSION AZ438336
VERSION AZ438336.1 GI:10562349
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
Dunn, D., Aoyagi, A., Barber, M., Bescorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0228 row: E column: 19

Seq primer: CCTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 38.
 Location/Qualifiers

FEATURES
 source

1.38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0228E19"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|9b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

Query Match 57.7%; Score 15; DB 17; Length 38;
 Best Local Similarity 78.3%; Pred. No. 2.1e+04;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23
 ||| ||| ||| ||| ||| |||
 Db 10 TGGCACATGCCCTTAATCCACG 32

RESULT 15
 AZ489704/c 41 bp DNA linear GSS 05-OCT-2000
 LOCUS 1M032211AF Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION
 ACCESSION
 AZ489704
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 41)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0322 row: L column: 14

Seq primer: CCTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 41.
 Location/Qualifiers

FEATURES
 source

1.41
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M032214"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|9b1AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

Query Match 57.7%; Score 15; DB 17; Length 41;
 Best Local Similarity 78.3%; Pred. No. 2.1e+04;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TGGTCATGCTTTGGTCCACG 23
 ||| ||| ||| ||| ||| |||
 Db 28 TGGTACATGCCCTTAATCCACG 6

Search completed: June 21, 2003, 23:58:52
 Job time : 1129.24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 602.344 seconds
(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-11

Perfect score: 30

Sequence: 1 ATCAACCTGGCGACATGTTGTAACCCCATC 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pal:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	62.0	47	6	AX378746 Sequence
2	17.8	59.3	24	6	AX183954 Sequence
3	17.4	58.0	29	6	A84718 Sequence 11
4	17.4	58.0	47	6	AX114379 Sequence
5	16.8	56.0	25	6	E50643 Simple dele
6	16.6	55.3	29	6	AX021753 Sequence
7	16.6	55.3	29	6	AX025434 Sequence
8	16.6	55.3	40	6	AX183780 Sequence
9	16.4	54.7	39	6	AX077406 Sequence
10	16.2	54.0	41	6	A34769 Sequence
11	16	53.3	34	6	A34738 Eglin seque
12	16	53.3	34	6	A34747 Modified Egl
13	15.2	50.7	31	6	AX249031 Sequence
14	15.2	50.7	37	6	AX425081 Sequence
15	15.2	50.7	47	6	AX114375 Sequence
16	15.2	50.7	50	6	AX322206 Sequence
17	15.2	50.0	41	6	AX330591 Sequence
18	15	50.0	41	6	AX268229 Sequence
19	15	50.0	41	6	AX268242 Sequence
20	15	50.0	42	6	A93509 Sequence 2
21	15	50.0	48	6	A93513 Sequence 6
22	15	50.0	48	6	A93514 Sequence 7
23	14.8	49.3	26	6	AR080211 Sequence
24	14.8	48.7	26	6	AR103647 Sequence
25	14.6	48.7	26	6	AX190637 Sequence
26	14.6	48.7	27	6	AX299931 Sequence
27	14.6	48.7	29	6	AX283139 Sequence
28	14.6	48.7	31	6	A76904 Sequence 10
29	14.6	48.7	31	6	I49720 Sequence 14
30	14.6	48.7	41	6	AX022217 Sequence
31	14.6	48.7	41	6	AX030743 Sequence
32	14.6	48.7	41	6	BD008658 Stable ex
33	14.4	48.0	37	6	AX192292 Sequence
34	14.2	47.3	19	12	AB069002 Synthetic
35	14.2	47.3	30	6	AX268952 Sequence
36	14.2	47.3	30	6	AX441224 Sequence
37	14.2	47.3	34	6	AR025212 Sequence
38	14.2	47.3	34	6	AR029059 Sequence
39	14.2	47.3	34	6	AR110630 Sequence
40	14.2	47.3	34	6	AX040099 Sequence
41	14.2	47.3	37	6	AX219952 Sequence
42	14.2	47.3	37	6	AX220037 Sequence
43	14.2	47.3	37	6	AX425140 Sequence
44	14.2	47.3	37	6	AX425148 Sequence
45	14	46.7	24	6	AX446233 Sequence

ALIGNMENTS

RESULT 1
AX378746/c AX378746 47 bp DNA linear PAT 18-MAR-2002
LOCUS Sequence 535 from Patent WO0206525.
DEFINITION AX378746
ACCESSION AX378746
VERSION AX378746.1 GI:19574599
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1. Cohen, D., Blumenfeld, M., Chumakov, I., Abderrahim, H. and Bihain, B.
Obesity associated biallelic marker maps
Patent: WO 0206525-A 535 24-JAN-2002;
JOURNAL

FEATURES	GENSET (FR)
SOURCE	Location/Qualifiers 1..47 /organism="Homo sapiens" /db_xref="taxon:9606"
Variation	24 /note="99-4582-359 : polymorphic base G or T"
BASE COUNT.	8 a 14 c 11 g 13 t 1 others
ORIGIN	
Query Match	Best Local Similarity 62.0%; Score 18.6; DB 6; Length 47; Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Oy	1 ATCAACTGGCGAACAATGTTGAACCCC 27 1 1 1 1 1 1 30 ACCATCMTGGTGTAAACGGTGTAACCC 4
Db	
RESULT 2	
AXI83954	
LOCUS	AXI83954 24 bp DNA linear PAT 06-AUG-2001D
DEFINITION	Sequence 1707 from Patent WO0142511.
ACCESSION	AXI83954
VERSION	AXI83954.1 GI:15135287
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 24) Daily,M., Hudson,T.J., Lander,E.S., Rloux,J. and Siminovitsh,K. Ibd-related polymorphisms Patent: WO 0142511-A 1707 14-JUN-2001; WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis Biotherapeutics Corporation (CA) location/Qualifiers 1..24 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	5 a 9 c 5 g 4 t 1 others
ORIGIN	
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OY	6 CCTGGCGAACATGCTGAACCCC 27 2 CCTGGCCACACTGCTGAACACC 23
Db	
RESULT 3	
AXI84718/c	
LOCUS	AXI84718 29 bp DNA linear PAT 21-JAN-2000
DEFINITION	Sequence 11 from Patent WO9844152.
ACCESSION	AXI84718
VERSION	AXI84718.1 GI:6733586
KEYWORDS	
SOURCE	unidentified. unclassified.
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 29) Farinelli,L. and Mayer,P. METHOD OF NUCLEIC ACID SEQUENCING Patent: WO 9844152-A 11 08-OCT-1998; FARINELLI LAURENT (CH); MAYER PASCAL (CH) location/Qualifiers 1..29 /organism="unidentified" /db_xref="taxon:32644"
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
SOURCE	
BASE COUNT	2 a 6 c 11 g 10 t
ORIGIN	

Query Match	Best Local	Matches		Score 17.4; Pred. No. 5.3e+03;	DB 6;	Length 29;
Similarity 77.8%;	Conservative 21;	Mismatches 0;	Indels 6;	Gaps 0;		
Oy	Db					
1 ATCAACCTGGCGAACATGTTGAACCCC 27	28 ACCAGCCTGCACCATGTGAGAACC 2					
RESULT 4	AXI14379			47 bp	DNA	Linear PAT 11-MAY-2001
LOCUS	Sequence	48 from Patent: WO0129257.				
DEFINITION	AXI14379					
KEYWORDS	AXI14379.1 GI:14031343					
SOURCE	human.					
ORGANISM	Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
REFERENCE	1 (bases 1 to 47)					
AUTHORS	SCHORK,N. and Skierczynski,B.					
TITLE	Methods of genetic cluster analysis and use thereof					
JOURNAL	Patent: WO 0129257-A 48 26-Apr-2001;					
GENSET (FR)						
FEATURES	Location/Qualifiers					
source	1..47					
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
Variation	24					
BASE COUNT	16 a 14 c 7 g 9 t 1 others					
ORIGIN						
Query Match	Best Local	Matches		Score 58.0%; Pred. No. 5.5e+03;	DB 6;	Length 47;
Similarity 77.8%;	Conservative 21;	Mismatches 0;	Indels 6;	Gaps 0;		
Oy	Db					
1 ATCAACCTGGCGAACATGTTGAACCCC 27	8 ACCATCTTGCTTACASAGTGAACCC 34					
RESULT 5	ES0643					
LOCUS	ES0643					
DEFINITION	Simple detection method of drug-metabolizing synthetase gene polymorphism.			25 bp	DNA	Linear PAT 31-JAN-2002
ACCESSION	ES0643					
VERSION	ES0643.1 GI:18629424					
KEYWORDS	JP 2001017185-A/7.					
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Mizugaki,M. and Hiratsuka,M.					
TITLE	Simple detection method of drug-metabolizing synthetase gene					
JOURNAL	Patent: JP 2001017185-A 7 23-JAN-2001;					
OS	OTSUKA PHARMACEUT CO LTD					
COMMENT	Unidentified					
PN	JP 2001017185-A/7					
PD	23-JAN-2001					
PF	10-DEC-1999 JP 1999351610					
PR						
PI	MICHIMAO MIZUGAKI, MASAHIRO HIRATSUKA					
PC	C12N15/09, C12Q1/68, C12N15/00					
CC						
FH	key					
FT	source					
FT	1..25					
	Location/Qualifiers					
	/organism='Unidentified'.					
FEATURES	Location/Qualifiers					
source	1..25					

```

BASE COUNT      6 a      7 c      6 g      6 t
ORIGIN

Query Match      56.0%; Score 16.8; DB 6; Length 25;
Best Local Similarity 90.0%; Pred. No. 9.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      8 TGGCGACATGCTGAACCC 27
      1 TGGCCACATGCTGAACCC 20
Db

RESULT 6
AX021753/c      AX021753      29 bp      DNA      linear      PAT 07-SEP-2000
LOCUS      Sequence 84 from Patent WO923221.
DEFINITION      AX021753
ACCESSION      AX021753
VERSION      AX021753.1 GI:10045009
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 29)
AUTHORS      Howell, S., Ledebuer, A.M., Frenken, L.G. and van der Logt, C.P.E.
TITLE      Multivalent antigen-binding proteins
JOURNAL      Patent: WO 923221-A 84 14-MAY-1999;
      HOWELL, STEVEN (GB); UNILEVER PLC (GB); LEDEBUER ADRIANUS MARINUS
      (NL); LOGT CORNELIS PAUL ERIK V D (NL); UNILEVER NV (NL); FRENKEN
      LEON GERARDUS JOSEPH (NL)
FEATURES
      source
      1..29
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="linker"

BASE COUNT      5 a      8 c      8 g      8 t
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 29;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ACCTGGCGAACAATGTAACCC 27
      26 ACCTGGTGAACCTGGAGAACAC 4
Db

RESULT 7
AX025434/c      AX025434      29 bp      DNA      linear      PAT 16-SEP-2000
LOCUS      Sequence 37 from Patent EP1002861.
DEFINITION      AX025434
ACCESSION      AX025434
VERSION      AX025434.1 GI:10187110
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      synthetic construct.
FEATURES      artificial sequences.
      source
      1..29
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="linker"

BASE COUNT      5 a      8 c      8 g      8 t
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 29;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 ACCTGGCGAACAATGTAACCC 27
      26 ACCTGGTGAACCTGGAGAACAC 4
Db

```

```

RESULT 8
AX183780
LOCUS      AX183780      40 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION      Sequence 1533 from Patent WO0142511.
ACCESSION      AX183780
VERSION      AX183780.1 GI:15135106
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS      Daly, M., Hudson, T.J., Lander, E.S., Rioux, J. and Siminovitch, K.
TITLE      1 (bases 1 to 40)
JOURNAL      Idb-related polymorphisms
      Patent: WO 0142511-A 1533 14-JUN-2001.
      WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); ELLIPSIS
      BIOTHERAPEUTICS CORPORATION (CA)
FEATURES      Location/Qualifiers
      source
      1..40
      /organism="Homo sapiens"
      /db_xref="taxon:9606"

BASE COUNT      13 a      7 c      12 g      7 t      1 others
ORIGIN

Query Match      55.3%; Score 16.6; DB 6; Length 40;
Best Local Similarity 82.6%; Pred. No. 1.2e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGAACAATGCTGAA 23
      17 ACCAGCCTGACTACATGCTGAA 39
Db

RESULT 9
AX077406/c      AX077406      39 bp      DNA      linear      PAT 22-FEB-2001
LOCUS      Sequence 19 from Patent WO0107640.
DEFINITION      AX077406
ACCESSION      AX077406
VERSION      AX077406.1 GI:13121956
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 39)
AUTHORS      Gill, P.T., Hussain, J.T. and Long, A.T.
TITLE      Improvements in and relating to analysis of dna
JOURNAL      Patent: WO 0107640-A 19 01-FEB-2001;
      The Secretary of State for the Home Department (GB)
FEATURES      Location/Qualifiers
      source
      1..39
      /organism="synthetic construct"
      /db_xref="taxon:32630"
      /note="A human Gc forward primer attached to an artificial
      universal primer tag to detect a SNP polymorphism at
      Cc1s/1f, page 48."

BASE COUNT      5 a      11 c      11 g      12 t
ORIGIN

Query Match      54.7%; Score 16.4; DB 6; Length 39;
Best Local Similarity 76.9%; Pred. No. 1.5e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      5 ACCTGGCGAACAATGTAACCCATC 30
      36 AACTGGCAAGCTGCTGAAGACATC 11
Db

RESULT 10
A34769
LOCUS      A34769      41 bp      DNA      linear      PAT 03-JUL-2002
DEFINITION      Synthetic eglin gene duplex.

```

ACCESSION	A34769
VERSION	A34769.1
KEYWORDS	GI:21694261
SOURCE	
ORGANISM	. synthetic construct. synthetic construct. artificial sequences.
REFERENCE	1 (bases 1 to 41)
AUTHORS	Rink,H., Liersch,M., Sieber,P., Rittel,W., Meyer,F., Seemüller,U., Fritz,H., Maerki,W. and Alkan,S. Process for the preparation of protease inhibitors Patent: EP 0146785-A 43 03-JUL-1985; CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG
TITLE	Location/Qualifiers
JOURNAL	1..41
FEATURES	/organism="synthetic construct" /db_xref="taxon:32630"
SOURCE	15 a 10 c 8 g 8 t
BASE COUNT	
ORIGIN	

Query Match	54.0%	Score 16.2	DB 6	length 41
Best Local Similarity	72.4%	Pred. No. 1	9e+04	
Matches	21	Conservative	0	Mismatches 8; Indels 0; Gaps 0.
QY	1	ATCAACCTGGCGAACATGTTGAACCCCAT	29	
Db	11	ACCAACATGCGCGAACATGTTAAACACCT	39	

RESULT	11								
LOCUS	A34738								
DEFINITION	A34738 34 bp DNA linear PAT 06-AUG-1996								
ACCESSION	A34738								
VERSION	A34738.1								
KEYWORDS	GI:1568271								
SOURCE	unidentified.								
ORGANISM	unclassified.								
REFERENCE	1 (bases 1 to 34)								
AUTHORS	Rink,H., Liersch,M., Sieber,P., Rittel,W., Meyer,F., Seemuller,U.,								
TITLE	Fritz,H., Maerkli,W. and Alkan,S.								
JOURNAL	Process for the preparation of protease inhibitors								
	Patent: EP 0146785-A 12 03-JUL-1985;								
	CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG								
FEATURES	Location/Qualifiers								
source	1..34								
	/organism="unidentified"								
	/db_xref="taxon:32644"								
BASE COUNT	12 a	9 c	7 g	6 t					
ORIGIN									

Query Match	53.3%	Score 16	DB 6	Length 34
Best Local Similarity	79.2%	Pred. No. 2.3e+04		
Matches 19	Conservative 0	Mismatches 5	Indels 0	Gaps 0
Oy	1 ATCAACCTGGCGACATGTTGAAC	24		
	.			
Db	11 ACCAACATGCGGAACATGTTTAAC	34		

RESULT	12
A34747/c	
LOCUS	A34747
DEFINITION	Modified Eglin C sequence.
ACCESSION	A34747
VERSION	A34747.1
KEYWORDS	GI:21694241
SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 34)
	Rink,H., Liersch,M., Sieber,P., Rittel,W., Meyer,F., Seemüller,U., Filtz,H., Maerkl,W. and Alkan,S.

TITLE	Process for the preparation of protease inhibitors									
JOURNAL	Patent: EP 0146785-A 21 03-JUL-1985;									
FEATURES	CIBA-GEIGY AG; PLANTORGAN WERK Heinrich G.E. Christensen KG									
SOURCE	1. .34 Location/Qualifiers									
BASE COUNT	/organism="unidentified" /db_xref="taxon:32644"									
ORIGIN	6 a 7 c 9 g 12 t									
Query Match	53.3%; Score 16; DB 6; Length 34;									
Best Local Similarity	79.2%; Pred. No. 2.3e+04;									
Matches	19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;									
OY	1 ATCAACCTGGGAGACATGCTGAAC 24 									
DB	24 ACCACACATGGCGAGACATGGTTAAC 1									

RESULT	13					
AX249031/c						
LOCUS	AX249031	31 bp	DNA			
DEFINITION	Sequence 1110 from Patent WO0166800.					
ACCESSION	AX249031					
VERSION	AX249031.1	GI:15865654				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
						PAT 28-SEP-2001

REFERENCE	1 (bases 1 to 31)				
AUTHORS	Cargill,M., Ireland,J.S. and Lander,E.S.				
TITLE	Human single nucleotide polymorphisms				
JOURNAL	Patent: WO 0166800-A 1110 13-SEP-2001;				
FEATURES	WHITHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)				
SOURCE	Location/Qualifiers				
	1..31				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
BASE COUNT	6 a	11 c	4 g	9 t	1 others
ORIGIN					

Query Match	50.7%	Score 15.2:	DB 6:	Length 31:
Best Local Similarity	77.3%	Pred. No. 5.1e+04:		
Matches	17:	Conservative	1:	Mismatches 4: Indels 0: Gaps 0:
QY	8	TGGCGACATGCTGACCCCAT	29	
		+ + + + + + + +		
Db	25	TGGTGTACAYGCTGAAGCCAA	4	

RESULT	14
AX425081/c	
LOCUS	AX425081 37 bp mRNA linear PAT 18-JUN-2002
DEFINITION	Sequence 3417 from patent WO0189124.
ACCESSION	AX425081
VERSION	AX425081.1 GI:21528463
KEYWORDS	.
SOURCE	synthetic construct.
ORGANISM	synthetic construct.
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Jarvis,T. von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randl,A.M.
JOURNAL	Method and reagent for the inhibition of erg Patent:WO 0189124-A 3417 22-NOV-2001;
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
source	location/Qualifiers
	1..37
	/organism="synthetic construct"
	/db_xref="taxon:32630"
	/note="Enzymatic Nucleic Acid"
	7 a 8 c 10 g 12 t
CASE COUNT	

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 164.531 seconds
(without alignments)
410.621 Million cell updates/sec

Title: US-09-964-666-11
Perfect score: 30
Sequence: 1 ATCAACCTGCGGACATGTGATGACCCATC 30

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.4	71.3	29	21	AAA03983
2	20.6	68.7	41	24	ABA01400
3	20.6	68.7	41	24	ABA01401
4	19.2	64.0	33	24	AAAS1589
5	19	63.3	41	24	ABLA9775
6	19	63.3	41	24	ABLA9776
7	19	63.3	47	21	AAZ65526
8	19	63.3	49	22	AAK65537
9	19	63.3	49	22	AAI62905

C	10	18.6	62.0	47	24	ABK41287	Human USP2 gene bi
C	11	18.4	61.3	29	21	AAA04485	Polymorphic fragme
C	12	18.2	60.7	33	24	ABK12114	Human EHD 9.57 pro
C	13	18.2	60.7	33	24	ABK14174	Insulin like growt
C	14	18.2	60.7	34	22	AAH27605	Human II aminoacyl
C	15	18	60.0	29	21	AAA04312	Polymorphic fragme
C	16	17.8	59.3	24	22	AAH91382	Human inflammatory
C	17	17.8	59.3	33	24	ABK01398	Human NF-E2-associ
C	18	17.6	58.7	41	24	ABK94080	Human multi-copper
C	19	17.6	58.7	41	24	ABK94081	Human multi-copper
C	20	17.4	58.0	33	22	AAI65108	Human hypoxia-indu
C	21	17.4	58.0	41	24	AAI43826	Human oncogene pro
C	22	17.4	58.0	41	24	AAI43827	Human oncogene pro
C	23	17.4	58.0	41	24	ABK96812	Human uteroglobin
C	24	17.4	58.0	41	24	ABK96813	Human uteroglobin
C	25	17.4	58.0	47	21	AAZ66299	Human map-related
C	26	17.4	58.0	47	22	AAH9248	Sample member clus
C	27	17.4	58.0	50	22	AAI28723	Human SNP oligonuc
C	28	17.2	57.3	29	21	AAA04311	Polymorphic fragme
C	29	17.2	57.3	33	24	ABK84112	Human protein 11.1
C	30	17	56.7	29	21	AAA04503	Polymorphic fragme
C	31	16.8	56.0	25	22	AAH84351	Human CYP2C18i PCR
C	32	16.6	55.3	24	24	ABK02134	Human zinc ion tra
C	33	16.6	55.3	29	21	AAH00661	Synthetic oligonuc
C	34	16.6	55.3	40	22	AAH91207	Human inflammatory
C	35	16.4	54.7	39	22	AAH74239	DNA analysis metho
C	36	16.4	54.7	41	24	AAH77547	Human red blood ce
C	37	16.2	54.0	22	21	AAH00662	Synthetic oligonuc
C	38	16.2	54.0	33	24	ABK49773	Human tyrosinase 1
C	39	16	53.3	33	24	ABK61326	Human pur-alpha 13
C	40	16	53.3	41	24	ABK47938	Corticotrophin rel
C	41	16	53.3	41	24	ABK47939	Corticotrophin rel
C	42	15.6	52.0	31	22	AAI30622	Human single nucle
C	43	15.6	52.0	33	24	ABK14188	Human splicing fac
C	44	15.6	52.0	33	24	ABK02347	Human pax protein
C	45	15.6	52.0	34	22	AAH46543	DNA polymerase 17

ALIGNMENTS

RESULT 1	AAA03983	standard: DNA; 29 BP.
ID	AAA03983	
AC	AAA03983:	
XX		
DT	22-MAY-2000	(first entry)
XX		
DE		Polymorphic fragment of hypertension associated gene APOC3.
XX		
KW		Polymorphism: hypertension; agammaglobulinemia; diabetes insipidus;
KW		Lesch-Nyhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
KW		Fabry's disease; familial hypercholesterolemia; hereditary spherocytosis;
KW		polycystic kidney disease; von Willebrand's disease; forensic; human;
KW		tubercous sclerosis; hereditary hemorrhagica telangiectasis;
KW		familial colonic polyposis; osteogenesis imperfecta; porphyria;
KW		Ehlers-Danlos syndrome; ss.
XX		
OS	Homo sapiens.	
XX		
PN	EP955382-A2.	
XX		
PD	10-NOV-1999.	
XX		
PF	07-MAY-1999.	99EP-0250150.
XX		
PR	07-MAY-1998:	98US-0084641.
XX		
PR	03-MAY-1999:	99US-0304232.
XX		
PA	(AFVY-) AFFYMETRIX INC.	
XX	(UYCA-) UNIV CASE WESTERN RESERVE.	

P1 Fan JB, Chakravarti A, Haluska MK;
 XX
 DR WPI: 2000-107928/10.
 XX
 XX Novel nucleic acids containing polymorphisms used in the diagnosis of
 PT hypertension -
 XX
 PS Claim 1; Page 22: 53pp: English

The invention provides polymorphic fragments of genes associated with hyperextension. The nucleic acids including the polymorphic sites can be used as probes or primers for expressing variant proteins. Detection of the polymorphisms is useful in designing prophylactic and therapeutic regimens customized to underlying abnormalities. The polymorphisms can be used for association studies for hyperextension, and in hyperextension diagnostic assays. Where the polymorphisms have strong correlation with hyperextension, within a gene, they are likely to have a causative role in hyperextension. This information can be used to find the precise role of polymorphism in the disease, and this can be used to identify potential drugs which combat the disease. The polymorphisms can be tested for association with other diseases e.g. agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial acrotic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria. The polymorphic forms can also be used in forensics to identify individuals.

50. Sequence 29 BP; 9 A; 11 C; 5 G; 3 T; 1 other;

Query Match	71.3%	Score 21.4	DB 21	Length 29	.
Best Local Similarity	88.0%	Pred. No. 14			
Matches 22; Conservative	1;	Mismatches	2;	Indels	0;
				Gaps	0;

QY	3	CAACCTGGCGAACATGGTGAACCCC	27
		:	
Db	1	CAACCTGGCGAACACAYGGTGAACCCC	25

RESULT 2
ABA01400/c
ID ABA01400 standard; DNA; 41 BP

DT 31-JAN-2002 (first entry)

Human NF-E2-associated factor 13 probe #1.

KM Human; NF- κ B-associated factor 13; cytosstatic; virucidal;
 KW immunomodulatory; antiinflammatory; haemostatic; gene therapy; tumour
 KW hemopathy; HIV infection; immunological disease; inflammation;
 KW developmental disorder; probe; ss.

OS Homo sapiens.

PN W0200175024-A2

PD 11-OCT-2001

PF 19-MAR-2001; 2001WO-CN00368

PR 22-MAR-2000; 2000CN-0115024.

PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR 'WPI; 2002-025846/03

PT Human NF-E2-associated factor 13 and encoded polynucleotide, applicable in diagnosis and treatment of e.g. malignant tumor, hemopathy, HIV

PT infection, immunological diseases and inflammation
XX
PS
Example 6; Page 15; 34pp; Chinese.

CC The present invention relates to human NF-E2-associated factor 13 (see
CC AM552544). The factor and its coding sequence are useful in the diagnosis
CC and treatment of malignant tumours, haemophathy, HIV infection,
CC immunological diseases, various inflammations and developmental
CC disorders. The present sequence is a probe, which was used in an
CC example from the present invention.

Sequence 41 BP; 7 A; 11 C; 13 G; 10 T; 0 other;

Query Match	Score 20.6;	DB 24;	Length 41;
Best Local Similarity	85.7%;	Pred No. 30;	
Matches 23; Conservative	0;	Mismatches 4;	Indels 0; Gaps 0

QY	1	ATCAACCTGGCGAACATGTTGAACCC	27
Db	29	ACCAGCCTGGCCAACATGTTGAACCC	3

RESULT 3
ABA01401/c
ID ABA01401 standard; DNA; 41 BP

AC ABA01401;

DT 31-JAN-2002 (first entry)

Human NF-E2-associated factor 13 probe #2.

KW Human; NF-E2-associated factor 3; cytosstatic; virucidal;
KW immunomodulatory; antiinflammatory; haemostatic; gene therapy; tumour
KW hamopathy; HIV infection; immunological disease; inflammation;
KW developmental disorder; probe; ss.

OS Homo sapiens.

PN WO200175024-A2.

PD 11-OCT-2001.

PF 19-MAR-2001; 2001WO-CN00368

PR 22-MAR-2000; 2000CN-0115024

PA (BLOW-) BLOWINDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

DR WPI; 2002-025846/03.

PT Human NF- κ B-associated factor 13 and encoded polynucleotide, applicable
PT in diagnosis and treatment of e.g. malignant tumor, hemopathy, HIV
PT infection, immunological diseases and inflammation -

PS Example 6; Page 15; 34pp; Chinese.

CC The present invention relates to human NF-E2-associated factor 13 (see
CC * [AM52544](#)). The factor and its coding sequence are useful in the diagnosis
CC and treatment of malignant tumours, haemopathy, HIV infection,
CC immunological diseases, various inflammations and developmental
CC disorders. The present sequence is a probe, which was used in an
CC example from the present invention.

Sequence 41 BP; 7 A; 11 C; 13 G; 10 T; 0 other;

Query Match	68.7%	Score 20.6;	DB 24;	Length 41;
-------------	-------	-------------	--------	------------

Matches	23;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

QY 1 ATCAACCTGGCGACATGCTGAACCC 27

DB 29 ACCAGCTGCGCCACATGCTGAACCC 3

RESULT 4

ID AAS15589 standard; DNA; 33 BP.

AC AAS15589;

DT 14-FEB-2002 (first entry)

DE Human DNA mismatch repair protein 10, PCR primer #2.

XX Human; DNA mismatch repair protein 10; cytostatic; virucidal;

KW immunomodulatory; anti-inflammatory; haemostatic; anti-HIV; inflammation;

KM human immunodeficiency virus; malignancy; haemopathy; infection;

OS immunological disease; PCR primer; ss.

XX Homo sapiens.

XX WO200175100-A1.

XX 11-OCT-2001.

XX 19-MAR-2001; 2001WO-CN00337.

XX 22-MAR-2000; 2000CN-0115057.

XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.

XX Mao Y, Xie Y;

XX WPI: 2002-025860/03.

XX New human DNA mismatch repair protein 10 for diagnosing and treating

PT malignancy, haemopathy, human immunodeficiency virus infection,

PS immunological diseases and inflammation

XX Example 4: Page 13; 36pp; Chinese.

CC The invention relates to an isolated polypeptide of human DNA mismatch

CC repair protein 10. The polypeptide can be used for screening mimics,

CC agonists, antagonists or inhibitors, or in peptide fingerprinting

CC identification. The polynucleotide can be used as primers for nucleic

CC acid amplification reactions, as probes for hybridisation reactions, or

CC in producing gene chips or microarrays. Drug compositions, which contain

CC the polypeptide, polynucleotide, mimics, agonists, antagonists,

CC inhibitors and their preparations, can be used treatment and

CC diagnosis of diseases relating to the polypeptide. In particular, the

CC polypeptide and encoded polynucleotide are applicable in diagnosis and

CC treatment of malignancy, haemopathy, human immunodeficiency virus (HIV)

CC infection, immunological diseases and various inflammations. The

CC present sequence represents PCR primer #2 used to amplify human DNA

CC mismatch repair protein 10.

SQ Sequence 33 BP; 9 A; 10 C; 8 G; 6 T; 0 other;

Query Match 64.0%; Score 19.2; DB 24: Length 33;

Best Local Similarity 87.5%; Pred. No. 1.1e+02;

Matches 21: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 TCACCTGCGCGAATGCTGAAC 25

DB 10 TCAGCTGCGCCACATGCTGAAC 33

RESULT 5

ABL49775/C

ID ABL49775 standard; DNA; 41 BP.

AC ABL49775;

XX

DT 29-MAY-2002 (first entry)

DE Human tyrosinase 10.34 probe 1 SEQ ID NO:8.

XX Human; tyrosinase; enzyme; human immunodeficiency virus infection;

KW HIV infection; cancer; probe; ss.

OS Homo sapiens.

XX CN1325972-A.

XX 12-DEC-2001.

XX 31-MAY-2000; 2000CN-0116261.

XX 31-MAY-2000; 2000CN-0116261.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI: 2002-196693/26.

XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer

PT and human immunodeficiency virus infection

PS Example 6: Page 19 (Disclosure); 32pp; Chinese.

XX The present invention describes human tyrosinase 10.34 (I). The present

CC invention also described a method for preparing (I) using DNA

CC recombination techniques. (I) and the polynucleotide encoding it can

CC be used in the treatment of diseases such as cancer and human

CC immunodeficiency virus (HIV) infection. The present sequence represents

CC a probe for human tyrosinase 10.34, which is used in an example from

CC the present invention.

SQ Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 other;

Query Match 63.3%; Score 19; DB 24: Length 41;

Best Local Similarity 81.5%; Pred. No. 1.4e+02;

Matches 22: Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATCACTGCGCGAATGCTGAACCC 27

DB 29 ACCAGCTGCGCCACATGCTGAACCC 3

RESULT 6

ABL49776/C

ID ABL49776 standard; DNA; 41 BP.

AC ABL49776;

XX 29-MAY-2002 (first entry)

XX Human tyrosinase 10.34 probe 2 SEQ ID NO:9.

DE Human; tyrosinase; enzyme; human immunodeficiency virus infection;

KW HIV infection; cancer; probe; ss.

OS Homo sapiens.

XX CN1325972-A.

XX 12-DEC-2001.

XX 31-MAY-2000; 2000CN-0116261.

XX 31-MAY-2000; 2000CN-0116261.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

```
XX WPI: 2002-196693/26.
DR
XX New polypeptide-tyrosinase 10.34 for treating diseases such as cancer
XX and human immunodeficiency virus infection
XX
XX Example 6; Page 19 (Disclosure): 32pp; Chinese.
XX
CC The present invention describes human tyrosinase 10.34 (I). The present
CC invention also described a method for preparing (I) using DNA
CC recombination techniques (I) and the polynucleotide encoding it can
CC be used in the treatment of diseases such as cancer and human
CC immunodeficiency virus (HIV) infection. The present sequence represents
CC a probe for human tyrosinase 10.34, which is used in an example from
CC the present invention.
XX
SQ Sequence 41 BP; 5 A; 12 C; 13 G; 11 T; 0 other;
XX
Query Match 63.3%; Score 19; DB 24; Length 41;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 ATCAACCTGCGCACATGCTGAACCC 27
Db 29 ACCAGCCCGCGCCACACATGCTGAACCC 3
RESULT 7
AAZ69526/c
ID AAZ69526 standard; DNA; 47 BP.
XX
XX AAZ69526;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:3882.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX variation replace(24,T)
XX /*tag=a
XX /standard_name="single nucleotide polymorphism"
XX
XX WO954500-A2.
XX
XX 28-OCT-1999.
XX
XX 21-APR-1999; 99WO-1B00822.
XX
XX 21-APR-1998; 98US-0082614.
XX
XX 23-NOV-1998; 98US-0109732.
XX
XX (GEST ) GENSET.
XX
XX Cohen D, Blumenfeld M, Chumakov I;
XX
XX WPI: 2000-013267/01.
XX
XX Novel diallelic markers used to construct a high density disequilibrium
XX map of the human genome
XX
XX Claim 3; Page 1058; 2745pp; English.
XX
XX AAZ65654 to AAZ69578 represent human diallelic markers from the present
XX invention, which contain a polymorphic base at position 24 of their
XX nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
XX primers for the diallelic markers. The diallelic markers of the
```

```
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 8 A; 14 C; 12 G; 13 T; 0 other;
XX
Query Match 63.3%; Score 19; DB 21; Length 47;
Best Local Similarity 81.5%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 ATCAACCTGCGCACATGCTGAACCC 27
Db 30 ACCATCTGCTGCTAACACGCTGAACCC 4
RESULT 8
AAK65537/c
ID AAK65537 standard; DNA; 49 BP.
XX
XX AAK65537;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20349.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX
XX 31-JAN-2000; 2000US-0179065.
XX
XX 04-FEB-2000; 2000US-0180628.
XX
XX 24-FEB-2000; 2000US-0184664.
XX
XX 02-MAR-2000; 2000US-0186350.
XX
XX 16-MAR-2000; 2000US-0189874.
XX
XX 17-MAR-2000; 2000US-0190076.
XX
XX 18-APR-2000; 2000US-0198123.
XX
XX 19-MAY-2000; 2000US-0205515.
XX
XX 07-JUN-2000; 2000US-0209467.
XX
XX 28-JUN-2000; 2000US-0214886.
XX
XX 30-JUN-2000; 2000US-0215135.
XX
XX 07-JUL-2000; 2000US-0216647.
XX
XX 07-JUL-2000; 2000US-0216880.
XX
XX 11-JUL-2000; 2000US-0217487.
XX
XX 11-JUL-2000; 2000US-0217496.
XX
XX 14-JUL-2000; 2000US-0218290.
XX
XX 26-JUL-2000; 2000US-0220963.
XX
XX 26-JUL-2000; 2000US-0220964.
XX
XX 14-AUG-2000; 2000US-0224518.
XX
XX 14-AUG-2000; 2000US-0224519.
XX
XX 14-AUG-2000; 2000US-0225213.
XX
XX 14-AUG-2000; 2000US-0225214.
XX
XX 14-AUG-2000; 2000US-0225266.
XX
XX 14-AUG-2000; 2000US-0225267.
XX
XX 14-AUG-2000; 2000US-0225268.
XX
XX 14-AUG-2000; 2000US-0225270.
XX
XX 14-AUG-2000; 2000US-0225447.
XX
XX 14-AUG-2000; 2000US-0225757.
```

PR 14-AUG-2000: 2000US-0225758.
 PR 14-AUG-2000: 2000US-0225759.
 PR 18-AUG-2000: 2000US-0226279.
 PR 22-AUG-2000: 2000US-0226681.
 PR 22-AUG-2000: 2000US-0226686.
 PR 23-AUG-2000: 2000US-0227182.
 PR 23-AUG-2000: 2000US-0227009.
 PR 30-AUG-2000: 2000US-0228924.
 PR 01-SEP-2000: 2000US-0229287.
 PR 01-SEP-2000: 2000US-0229343.
 PR 01-SEP-2000: 2000US-0229344.
 PR 01-SEP-2000: 2000US-0229345.
 PR 05-SEP-2000: 2000US-0229509.
 PR 05-SEP-2000: 2000US-0229513.
 PR 06-SEP-2000: 2000US-0230437.
 PR 06-SEP-2000: 2000US-0230438.
 PR 08-SEP-2000: 2000US-0231242.
 PR 08-SEP-2000: 2000US-0231243.
 PR 08-SEP-2000: 2000US-0231244.
 PR 08-SEP-2000: 2000US-0231413.
 PR 08-SEP-2000: 2000US-0231414.
 PR 08-SEP-2000: 2000US-0232080.
 PR 08-SEP-2000: 2000US-0232081.
 PR 12-SEP-2000: 2000US-0231968.
 PR 14-SEP-2000: 2000US-0232397.
 PR 14-SEP-2000: 2000US-0232398.
 PR 14-SEP-2000: 2000US-0232399.
 PR 14-SEP-2000: 2000US-0232400.
 PR 14-SEP-2000: 2000US-0232401.
 PR 14-SEP-2000: 2000US-0233063.
 PR 14-SEP-2000: 2000US-0233064.
 PR 14-SEP-2000: 2000US-0233065.
 PR 21-SEP-2000: 2000US-0234223.
 PR 21-SEP-2000: 2000US-0234274.
 PR 25-SEP-2000: 2000US-0234997.
 PR 25-SEP-2000: 2000US-0234998.
 PR 26-SEP-2000: 2000US-0235484.
 PR 27-SEP-2000: 2000US-0235834.
 PR 27-SEP-2000: 2000US-0235836.
 PR 29-SEP-2000: 2000US-0236327.
 PR 29-SEP-2000: 2000US-0236367.
 PR 29-SEP-2000: 2000US-0236368.
 PR 29-SEP-2000: 2000US-0236369.
 PR 29-SEP-2000: 2000US-0236370.
 PR 02-OCT-2000: 2000US-0236802.
 PR 02-OCT-2000: 2000US-0237037.
 PR 02-OCT-2000: 2000US-0237038.
 PR 02-OCT-2000: 2000US-0237039.
 PR 02-OCT-2000: 2000US-0237040.
 PR 13-OCT-2000: 2000US-0239935.
 PR 13-OCT-2000: 2000US-0239937.
 PR 20-OCT-2000: 2000US-0240960.
 PR 20-OCT-2000: 2000US-0241221.
 PR 20-OCT-2000: 2000US-0241785.
 PR 20-OCT-2000: 2000US-0241786.
 PR 20-OCT-2000: 2000US-0241787.
 PR 20-OCT-2000: 2000US-0241808.
 PR 20-OCT-2000: 2000US-0241809.
 PR 20-OCT-2000: 2000US-0241826.
 PR 01-NOV-2000: 2000US-0244617.
 PR 08-NOV-2000: 2000US-0246474.
 PR 08-NOV-2000: 2000US-0246475.
 PR 08-NOV-2000: 2000US-0246476.
 PR 08-NOV-2000: 2000US-0246477.
 PR 08-NOV-2000: 2000US-0246478.
 PR 08-NOV-2000: 2000US-0246523.
 PR 08-NOV-2000: 2000US-0246524.
 PR 08-NOV-2000: 2000US-0246525.
 PR 08-NOV-2000: 2000US-0246526.
 PR 08-NOV-2000: 2000US-0246527.
 PR 08-NOV-2000: 2000US-0246528.
 PR 08-NOV-2000: 2000US-0246532.
 PR 08-NOV-2000: 2000US-0246609.

PR 08-NOV-2000: 2000US-0246610.
 PR 08-NOV-2000: 2000US-0246611.
 PR 08-NOV-2000: 2000US-0246613.
 PR 17-NOV-2000: 2000US-0249207.
 PR 17-NOV-2000: 2000US-0249208.
 PR 17-NOV-2000: 2000US-0249209.
 PR 17-NOV-2000: 2000US-0249210.
 PR 17-NOV-2000: 2000US-0249211.
 PR 17-NOV-2000: 2000US-0249212.
 PR 17-NOV-2000: 2000US-0249213.
 PR 17-NOV-2000: 2000US-0249214.
 PR 17-NOV-2000: 2000US-0249215.
 PR 17-NOV-2000: 2000US-0249216.
 PR 17-NOV-2000: 2000US-0249217.
 PR 17-NOV-2000: 2000US-0249218.
 PR 17-NOV-2000: 2000US-0249244.
 PR 17-NOV-2000: 2000US-0249245.
 PR 17-NOV-2000: 2000US-0249245.
 PR 17-NOV-2000: 2000US-0249264.
 PR 17-NOV-2000: 2000US-0249265.
 PR 17-NOV-2000: 2000US-0249297.
 PR 17-NOV-2000: 2000US-0249299.
 PR 17-NOV-2000: 2000US-0249300.
 PR 01-DEC-2000: 2000US-0250160.
 PR 01-DEC-2000: 2000US-0250391.
 PR 05-DEC-2000: 2000US-0251030.
 PR 05-DEC-2000: 2000US-0251988.
 PR 05-DEC-2000: 2000US-0256719.
 PR 06-DEC-2000: 2000US-0251479.
 PR 08-DEC-2000: 2000US-0251856.
 PR 08-DEC-2000: 2000US-0251856.
 PR 08-DEC-2000: 2000US-0251868.
 PR 08-DEC-2000: 2000US-0251869.
 PR 08-DEC-2000: 2000US-0251889.
 PR 08-DEC-2000: 2000US-0251989.
 PR 11-DEC-2000: 2000US-0254097.
 PR 05-JAN-2001: 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis.
 PT
 XX
 PS Disclosure; SEQ ID NO 20349; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AM82170 to AM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patients own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AM82169
 CC represent sequences used in the exemplification of the present invention.
 CC
 XX
 SO Sequence 49 BP; 11 A; 12 C; 13 G; 13 T; 0 other;
 Query Match 63.3%; Score 19; DB 22; Length 49;
 Best Local Similarity 81.5%; Pred. No. 1,4e+02;
 Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 1 ATCAACCTGGCGAACATGTTGAACCCC 27

	Db	34	ACCATCTCGGCTAAATGCAGCAACC	8
RESULT 9	AAI62905	ID	AAI62905 standard; DNA; 49 BP.	
XX AC AAI62905;				
XX DT 22-OCT-2001 (first entry)				
XX DE Human genomic DNA SEQ ID NO 233.				
XX KW Humana; neotropic; neuroinfective; cytostatic; dermatological; virucide;				
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;				
KW antiparkinsonian; antisickling; antlanemic; antiarthritic; cancer;				
KW antifluemetic; hepatotoxic; cerebroprotective; antiinflammatory;				
KW antidiabetic; antituberc; anticancer; antiviral; antifungal;				
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;				
KW neurological disease; infection; nephrotoxic; gene therapy; vaccine;				
ds.				
XX OS Homo sapiens.				
XX PN W0200155449-A1.				
XX PD 02-AUG-2001.				
XX PF 17-JAN-2001; 2001MO-USO1346.				
XX PR 31-JAN-2000; 2000US-0179065.				
PR 04-FEB-2000; 2000US-0180628.				
PR 19-MAY-2000; 2000US-0205515.				
PR 07-JUL-2000; 2000US-0216880.				
PR 14-JUL-2000; 2000US-0218290.				
PR 14-AUG-2000; 2000US-0225447.				
PR 01-SEP-2000; 2000US-0229343.				
PR 06-SEP-2000; 2000US-0230437.				
PR 08-SEP-2000; 2000US-0231243.				
PR 25-SEP-2000; 2000US-0234997.				
PR 29-SEP-2000; 2000US-0236367.				
PR 13-OCT-2000; 2000US-0239937.				
PR 08-NOV-2000; 2000US-0246476.				
PR 08-NOV-2000; 2000US-0246477.				
PR 08-NOV-2000; 2000US-0246525.				
PR 08-NOV-2000; 2000US-0246526.				
PR 08-NOV-2000; 2000US-0246528.				
PR 17-NOV-2000; 2000US-0249210.				
PR 17-NOV-2000; 2000US-0249211.				
PR 17-NOV-2000; 2000US-0249214.				
PR 17-NOV-2000; 2000US-0249265.				
PR 01-DEC-2000; 2000US-0250160.				
PR 01-DEC-2000; 2000US-0250391.				
PR 05-DEC-2000; 2000US-0251030.				
PR 05-DEC-2000; 2000US-0251988.				
PR 05-DEC-2000; 2000US-0256719.				
PR 06-DEC-2000; 2000US-0251479.				
PR 08-DEC-2000; 2000US-0251989.				
PR 08-DEC-2000; 2000US-0251990.				
PR 11-DEC-2000; 2000US-0254097.				
PA (HUMA-) HUMAN GENOME SCI INC.				
PI Rosen CA, Barash SC, Ruben SM;				
XX WP1; 2001-476225/51.				
XX DR Novel plasma membrane associated proteins useful for diagnosing,				
XX PT treating, preventing and/or prognosing disorders related to the				
PT proteins, including cancer, immune response and neuronal disorders -				
XS Example 2; SEQ ID NO 233; 532bp + Sequence Listing; English.				

xx	The invention relates to novel genes (AA162752-AA162961) and proteins
cc	(AAW42347-AAW42415) useful for preventing, treating or ameliorating
cc	medical conditions e.g. by protein or gene therapy. The genes are
cc	isolated from a range of human tissues disclosed in the specification.
cc	The nucleic acids, proteins, antibodies and (ant)agonists are useful
cc	in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
cc	and ovarian cancer and other cancers of the adrenal gland, bone, bone
cc	marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
cc	(b) immune disorders e.g. Addison's disease, allergies, autoimmune
cc	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
cc	disease, multiple sclerosis, rheumatoid arthritis and ulcerative
cc	colitis; (c) cardiovascular disorders such as myocardial ischaemias;
cc	(d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
cc	epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
cc	and parasitic infections.
cc	Note: The sequence data for this patent did not form part of the
cc	printed specification, but was obtained in electronic format directly
cc	from WIPO at:ftp.wipo.int/pub/published_pct_sequences.
xx	
so	Sequence 49 BP; 13 A; 13 C; 12 G; 11 T; 0 Other;
	Query Match 63.3%; Score 19; DB 22; Length 49;
	Best Local Similarity 81.5%; Pred. No. 1.4e+02;
	Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Oy	1 ATCAACCTGGCCAACATGTTGAACCC 27
Db	16 ACCATCGTCGTAAAGTGTGAACCC 42
RESULT 10	
ABK41287/c	
ID	ABK41287 standard; DNA: 47 BP.
AC	
xx	ABK41287:
xx	
xx	21-MAY-2002 (first entry)
DE	
xx	Human USF2 gene biallelic marker.
KW	Human: obesity associated-biallelic marker; ds; LSR: USP2;
KW	drug response; hyperuricaemia; digestive pathology; hypertension; cancer;
KW	hepatic function disorder; cardiovascular disease; hyperlipidaemia;
KW	insulin disorder; atheromatous disease; cardiac insufficiency; obesity.
OS	Homo sapiens.
xx	
PN	WO200206525-A2.
xx	
PD	24-JAN-2002.
xx	
PF	28-JUN-2001; 2001WO-1B01477.
xx	
PR	18-JUL-2000; 2000US-219704P.
xx	
PA	(GEST) GENSET.
Pt	
Cohen D,	Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;
WIPI:	2002-155043/20.
Set of novel map-related biallelic markers, preferably located on	
obesity disorder-associated chromosomal regions on chromosomes 3, 10	
and 19, useful, for e.g. detecting statistical correlations between	
marker allele and a phenotype -	
Example 23; Page 302; 31pp; English.	
The invention relates to a set of novel map-related biallelic markers,	
preferably located on obesity disorder-associated chromosomal regions on	
chromosomes 3, 10 and 19. The markers are useful for genotyping or	
estimating the frequency of an allele in a population, for detecting an	

DB	31	ACCACCTGGCCACATGATGTGAA	9
DB	RESULT 13		
XX	ABK14174/c		
XX	ID	ABK14174 standard; DNA; 33 BP.	
XX	AC		
XX	ABK14174;		
XX	DT	21-MAY-2002 (first entry)	
XX	DE		
XX	DE	Insulin like growth factor binding protein 11.88 cDNA PCR primer #2.	
XX	XX		
XX	XX	Insulin like growth factor binding protein 11.88; primer: ss; cytosstatic;	
XX	KW	embryo development dysmorphia; malignant tumour; gene therapy; cancer;	
XX	KW	PCR.	
XX	OS	Unidentified.	
XX	PN	WO200212493-A1.	
XX	PD		
XX	PD	14-FEB-2002.	
XX	XX		
XX	PF	11-JUN-2001; 2001WO-CN00951.	
XX	PR		
XX	PR	14-JUN-2000; 2000CN-0116491.	
XX	PA	(BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.	
XX	PI		
XX	PI	Mao Y, Xie Y.	
XX	DR	WPI: 2002-172159/72.	
XX	XX		
XX	PT	Insulin like growth factor binding protein 11.88 and encoding	
XX	PS	polynucleotide, used in diagnosis and treatment of malignant tumours -	
XX	XX	Example 4; Page 13; 38pp; Chinese.	
XX	CC		
XX	CC	The invention relates to an insulin like growth factor binding protein	
XX	CC	11.88 and the DNA sequence encoding the polypeptide. The DNA and protein	
XX	CC	are used in diagnosis and treatment of malignant tumour and dysmorphia of	
XX	CC	development of an embryo. This sequence represents a PCR primer used for	
XX	CC	cloning of cDNA which encodes the insulin like growth factor binding	
XX	CC	protein 11.88 of the invention.	
XX	XX		
XX	XX	Sequence 33 BP; 5 A; 11 C; 8 G; 9 T; 0 other;	
XX	XX		
XX	XX	Query Match	60.7%; Score 18.2; DB 24; Length 33;
XX	XX	Best Local Similarity	87.0%; Pred. No. 2.9e+02;
XX	XX	Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0
XX	QY		
XX	1	ATCAACCTGGCGACATGATGTGAA	23
XX	1	111111111111111111111111	
XX	31	ACCACCTGGCCACATGATGTGAA	9
XX	DB		
XX	XX		
XX	XX	RESULT 14	
XX	XX	AAH27605/c	
XX	XX	ID	AAH27605 standard; DNA; 34 BP.
XX	XX	AAH27605;	
XX	XX		
XX	XX	31-AUG-2001 (first entry)	
XX	XX		
XX	XX	Human II aminoacyl-tRNA synthetase 9 PCR primer 4.	
XX	XX		
XX	XX	Human: II aminoacyl-tRNA synthetase 9; cytosstatic; antiviral;	
XX	XX	immunomodulatory; antiinflammatory; cancer; haemopathy;	
XX	XX	human immunodeficiency virus; HIV; infection; immunological disease;	
XX	XX	inflammatory disease; PCR primer; ss.	
XX	XX		
XX	XX	Homo sapiens.	
XX	XX		

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PN W0200140467-A1.
XX
XX 07-JUN-2001.
XX
XX 27-NOV-2000; 2000MO-CN00512.
XX
XX 30-NOV-1999; 99CN-0124170.
XX
XX (BIOR-) BIORAD GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2001-374843/39.
XX
XX Human II aminoacyl-tRNA synthase 9 and encoded polynucleotide, useful
XX in diagnosis and treatment of malignant tumor, hemopathy, HIV
XX infection, immunological diseases and various inflammation -
XX
XX Example 4; Page 13; 38pp; Chinese.
XX
XX The invention relates to an isolated polypeptide of human II
XX aminoacyl-tRNA synthase 9. The polypeptide comprises the 86 amino
XX acid sequence defined in the specification, or its fragment, analogue
XX or derivative. The polypeptide and the polynucleotide encoding it are
XX useful in the diagnosis and treatment of malignant tumours, haemopathy,
XX HIV infection, immunological diseases and various inflammatory diseases.
XX The polynucleotide is useful as a primer for nucleic acid amplification
XX reactions or as a probe for hybridisation reactions, or in producing gene
XX chips or microarrays. The polypeptide is useful for screening mimics,
XX agonists, antagonists or inhibitors, or for use in peptide fingerprinting
XX identification. The present sequence is a primer which was used to
XX amplify the polynucleotide encoding the polypeptide of the invention.
XX
XX Sequence 34 BP; 6 A; 11 C; 7 G; 10 T; 0 other;
XX
XX Query Match 60.7%; Score 18.2; DB: 22; Length 34;
XX Best Local Similarity 87.0%; Pred. No. 2.9e+02;
XX Matches 20; Conservative 0; Mismatches 3; Indels 0, Gaps 0
XX
OY 1 ATCAACCTGGCGACATGATGAA 23
XX | | | | | | | | | | | | | |
DB 31 ACCACCTGGCGTACATGATGAA 9
XX
RESULT 15
XX AAA04312/C
XX AAA04312 standard; DNA; 29 BP.
XX
XX AAA04312;
XX
XX 22-MAY-2000 (first entry)
XX
XX Polymorphic fragment of hypertension associated gene GLUT4.
XX
XX Leech-Myhan syndrome; muscular dystrophy; Wiskott-Aldrich syndrome;
XX Fabrys disease; familial hypercholesterolemia; hereditary spherocytosis;
XX polycystic kidney disease; von Willebrands disease; forensic human;
XX tuberosus sclerosis; hereditary hemorrhagica telangiectasia;
XX familial colonic polyposis; osteogenesis imperfecta; porphyria;
XX Ehlers-Danlos syndrome; ss.
XX
XX Homo sapiens.
XX
XX EP955382-A2.
XX
XX 10-NOV-1999.
XX
XX 07-MAY-1999; 99EP-0250150.
XX
XX 07-MAY-1998; 98US-0084641.
XX
XX 03-MAY-1999; 99US-0304232.
XX

```


PA (AFRY-) AFFYMETRIX INC.
PA (UYCA-) UNIV CASE WESTERN RESERVE.

XX
XX
PI Fan JB, Chakravarti A, Haluska MK;

XX
XX
DR WPI: 2000-107928/10.

XX
XX
PT Novel nucleic acids containing polymorphisms used in the diagnosis of
XX hypertension -

PS Claim 1; Page 32; 53pp: English.

XX
XX
CC The invention provides polymorphic fragments of genes associated with
CC hypertension. The nucleic acids including the polymorphic sites can be
CC used as probes or primers for expressing variant proteins. Detection of
CC the polymorphisms is useful in designing prophylactic and therapeutic
CC regimes customized to underlying abnormalities. The polymorphisms can be
CC used for association studies for hypertension, and in hypertension
CC diagnostic assays. Where the polymorphisms have strong correlation with
CC hypertension, within a gene, they are likely to have a causative role in
CC hypertension. This information can be used to find the precise role of a
CC polymorphism in the disease, and this can be used to identify potential
CC drugs which combat the disease. The polymorphisms can be tested for
CC association with other diseases e.g. agammaglobulinemia, diabetes
CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich
CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
CC acute intermittent porphyria. The polymorphic forms can also be used in
CC forensics to identify individuals.

XX
SQ Sequence 29 BP; 5 A; 7 C; 7 G; 9 T; 1 other;

Query Match 60.0%; Score 18; DB 21; Length 29;
Best Local Similarity 80.8%; Pred. No. 3.4e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATCAACCTGGCGACATGATGTAACCC 26
DB 26 ACCATCTGCGCYAACATGATGTAACCC 1

Search completed: June 21, 2003, 22:26:22
Job time : 165.531 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 35.625 Seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-11
Perfect score: 30
Sequence: 1 ATCAACCTGCGACATGTGTAACCCATC 30

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	62.0	47	4	US-09-641-638-659 Sequence 659, App
2	15.2	50.7	20	4	US-09-280-805-259 Sequence 259, App
3	15	50.0	42	4	US-09-171-425-2 Sequence 2, Appl
4	15	50.0	48	4	US-09-171-425-6 Sequence 6, Appl
5	15	50.0	48	4	US-09-171-425-7 Sequence 7, Appl
6	14.8	48.3	26	2	US-08-747-535-17 Sequence 17, Appl
7	14.8	48.3	29	3	US-09-009-913-171 Sequence 171, App
8	14.6	48.7	31	1	US-08-256-368-14 Sequence 14, App
9	14.6	48.7	41	4	US-09-297-269-36 Sequence 36, Appl
10	14.4	48.0	30	1	US-07-718-490-2 Sequence 2, Appl
11	14.4	48.0	50	1	US-07-718-490-1 Sequence 1, Appl
12	14.2	47.3	34	1	US-08-471-496-7 Sequence 7, Appl
13	14.2	47.3	34	2	US-08-894-840-7 Sequence 7, Appl
14	14.2	47.3	34	3	US-09-139-675-7 Sequence 7, Appl
15	14	46.7	28	4	US-08-853-774-11 Sequence 11, Appl
16	14	46.7	33	3	US-08-469-318-171 Sequence 171, App
17	14	46.7	33	3	US-08-468-609A-171 Sequence 171, App
18	14	46.7	33	3	US-08-471-045-53 Sequence 53, Appl
19	14	46.7	33	3	US-08-469-712A-53 Sequence 53, Appl
20	14	46.7	33	4	US-08-875-533-26 Sequence 26, Appl
21	14	46.7	33	4	US-08-446-871-53 Sequence 53, Appl
22	14	46.7	33	4	US-08-446-872A-171 Sequence 171, App
23	14	46.7	33	4	US-08-468-910-53 Sequence 53, Appl
24	14	46.7	33	4	US-08-761-907-53 Sequence 53, Appl
25	14	46.7	33	4	US-08-762-227A-171 Sequence 171, App
26	14	46.7	33	5	PCT-US95-01185-171 Sequence 171, App
27	14	46.7	37	4	US-09-344-888A-19 Sequence 19, Appl

C 28	14	46.7	38	1	US-08-642-255-22 Sequence 22, Appl
C 29	14	46.7	38	3	US-08-475-411A-53 Sequence 53, Appl
C 30	14	46.7	38	4	US-08-478-029A-53 Sequence 53, Appl
C 31	13.8	46.0	20	1	US-07-991-199D-14 Sequence 14, Appl
C 32	13.8	46.0	20	4	US-09-593-589-81 Sequence 81, Appl
C 33	13.8	46.0	30	4	US-08-870-511-28 Sequence 28, Appl
C 34	13.8	46.0	43	1	US-08-766-014-10 Sequence 10, Appl
C 35	13.8	46.0	46	4	US-08-707-860D-1 Sequence 1, Appl
C 36	13.6	45.3	21	3	US-09-159-274-22 Sequence 22, Appl
C 37	13.6	45.3	30	1	US-07-789-179-7 Sequence 7, Appl
C 38	13.6	45.3	30	1	US-08-240-712-16 Sequence 16, Appl
C 39	13.6	45.3	30	1	US-08-443-890-16 Sequence 16, Appl
C 40	13.6	45.3	30	1	US-08-444-942-7 Sequence 7, Appl
C 41	13.6	45.3	30	1	US-08-444-942-7 Sequence 7, Appl
C 42	13.6	45.3	30	1	US-08-444-939-7 Sequence 7, Appl
C 43	13.6	45.3	30	2	US-08-444-991-7 Sequence 7, Appl
C 44	13.6	45.3	30	2	US-08-450-733-7 Sequence 7, Appl
C 45	13.6	45.3	30	4	US-09-058-562-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-641-638-659
Sequence 659, Application US/09641638
Patent No. 6432648

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetel, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051CPI
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/641,638
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO: 659
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-520-256 : polymorphic base C or T
US-09-641-638-659

Query Match
Best Local Similarity 77.8%; Score 18.6; DB 4; Length 47;
Matches 21; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

DB 17 ACCATCTGCGTACACGCGTGAACCC 43

RESULT 2
US-09-280-805-259
Sequence 259, Application US/09280805
Patent No. 6184212
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia

```
? TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
? TITLE OF INVENTION: EXPRESSION
? NUMBER OF SEQUENCES: 271
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Law Offices of Jane Massey Licata
? STREET: 66 East Main Street
? CITY: Marlton
? STATE: NJ
? COUNTRY: U.S.A.
? ZIP: 08053
? COMPUTER READABLE FORM:
? MEDIA TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
? COMPUTER: IBM PC
? OPERATING SYSTEM: WINDOWS 95
? SOFTWARE: WORDPERECT 6.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/280,805
? FILING DATE: herewith
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 09/048,810
? FILING DATE: March 26, 1998
? ATTORNEY/AGENT INFORMATION:
? NAME: Licata, Jane Massey
? REGISTRATION NUMBER: 32,257
? REFERENCE/DOCKET NUMBER: ISPH-0346
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 609-810-1515
? TELEFAX: 609-810-1454
? INFORMATION FOR SEQ ID NO: 259:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 20 base pairs
? TYPE: Nucleic Acid
? STRANDEDNESS: Single
? TOPOLOGY: Linear
? ANTI-SENSE: Yes
? US-09-280-805-259

Query Match          50.7%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 TGGCGAACAATGGTGAACCC 27
        ||||| ||||| ||||| |||||
DB      1 TGGCTAACACGCGTGAACCC 20

RESULT 3
US-09-171-425-2
? Sequence 2, Application US/09171425A
? Patent No. 6465438
? GENERAL INFORMATION:
? APPLICANT: Schorr, Joachim
? APPLICANT: Baker, Henry J.
? APPLICANT: Smith, Bruce F.
? TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
? FILE REFERENCE: 08909/003001
? CURRENT APPLICATION NUMBER: US/09/171,425A
? CURRENT FILING DATE: 1998-10-19
? EARLIER APPLICATION NUMBER: PCT/EP97/01943
? EARLIER FILING DATE: 1996-04-19
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 42
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetically generated oligonucleotides
? US-09-171-425-2

Query Match          50.0%; Score 15; DB 4; Length 42;
Best Local Similarity 78.3%; Pred. No. 7.6e+02;
Matches 78; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGAACAATGGTGAA 23
        ||||| ||||| ||||| |||||
DB      13 ATCAACCTGGCTAAGAGAAGAA 35

RESULT 4
US-09-171-425-6
? Sequence 6, Application US/09171425A
? Patent No. 6465438
? GENERAL INFORMATION:
? APPLICANT: Schorr, Joachim
? APPLICANT: Baker, Henry J.
? APPLICANT: Smith, Bruce F.
? TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
? FILE REFERENCE: 08909/003001
? CURRENT APPLICATION NUMBER: US/09/171,425A
? CURRENT FILING DATE: 1998-10-19
? EARLIER APPLICATION NUMBER: PCT/EP97/01943
? EARLIER FILING DATE: 1996-04-19
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 6
? LENGTH: 48
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetically generated oligonucleotides
? US-09-171-425-6

Query Match          50.0%; Score 15; DB 4; Length 48;
Best Local Similarity 78.3%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 ATCAACCTGGCGAACAATGGTGAA 23
        ||||| ||||| ||||| |||||
DB      19 ATCAACCTGGCTAAGAGAAGAA 41

RESULT 5
US-09-171-425-7/c
? Sequence 7, Application US/09171425A
? Patent No. 6465438
? GENERAL INFORMATION:
? APPLICANT: Schorr, Joachim
? APPLICANT: Baker, Henry J.
? APPLICANT: Smith, Bruce F.
? TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
? FILE REFERENCE: 08909/003001
? CURRENT APPLICATION NUMBER: US/09/171,425A
? CURRENT FILING DATE: 1998-10-19
? EARLIER APPLICATION NUMBER: PCT/EP97/01943
? EARLIER FILING DATE: 1996-04-19
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 7
? LENGTH: 48
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetically generated oligonucleotides
? US-09-171-425-7

Query Match          50.0%; Score 15; DB 4; Length 48;
Best Local Similarity 78.3%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```

RESULT 6
US-08-747-536-17
; Sequence 17, Application US/08747536
; Patent No. 5968737
; GENERAL INFORMATION:
; APPLICANT: Ali-Osman, Francis
; APPLICANT: Lopez-Berestein, Gabriel
; APPLICANT: Buolamwini, John
; APPLICANT: Antoun, Gamil
; APPLICANT: Lo, Hui-Men
; APPLICANT: Keller, Charles
; APPLICANT: Akande, Olanike
; TITLE OF INVENTION: GLUTATHIONE S-TRANSFERASE (GST) GENES IN
; TITLE OF INVENTION: CANCER
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,536
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-747-536-17

Query Match          49.3%; Score 14.8; DB 2; Length 26;
Best Local Similarity 88.9%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      6 CCTGGCAACATGCTGAA 23
        ||||| | |||||
Db      5 CCTGGTGCACATGCTGAA 22

RESULT 7
US-09-009-913-171
; Sequence 171, Application US/09009913
; Patent No. 6087485
; GENERAL INFORMATION:
; APPLICANT: Axy's Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ashtma Related Genes
; NUMBER OF SEQUENCES: 339
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Ave, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

```

```

; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,913
; FILING DATE: 21-JAN-1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: SEQ-4P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3231
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-009-913-171

Query Match          49.3%; Score 14.8; DB 3; Length 29;
Best Local Similarity 88.9%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      6 CCTGGCAACATGCTGAA 23
        ||||| | |||||
Db      9 CCTGGCTAACACGCTGAA 26

RESULT 8
US-08-256-368-14/c
; Sequence 14, Application US/08256368
; Patent No. 5641649
; GENERAL INFORMATION:
; APPLICANT: Stanchi, Ombretta
; APPLICANT: Negro, Alessandro
; APPLICANT: Callegaro, Lanfranco
; TITLE OF INVENTION: Expression Of Osteogenic Factor Op-1
; TITLE OF INVENTION: In Cells Of Spodoptera Frugiperda Infected With
; TITLE OF INVENTION: Recombinant Baculovirus
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,368
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 259-243P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)205-8000
; TELEFAX: (703)205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs

```

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PCR primer"
HYPOTHETICAL: NO
ANTI-SENSE: NO
US:08-256-368-14

Query Match 48.7%; Score 14.6; DB 1; Length 31;
Best Local Similarity 69.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2 TCACCTGGCAGACATGTGAACCCCATC 30
||| ||||| ||| ||||| ||| |||
Db 30 TCACCTGGCAGACAGAGTGCATCGACC 2

RESULT 9

US-09-297-269-36
Sequence 36, Application US/09297269
Patent No. 6451557

GENERAL INFORMATION:
APPLICANT: VAUGHAN, Paul R.
APPLICANT: GALANTIS, Maria
APPLICANT: RAMSHAW, John A.M.
APPLICANT: WERKMEISTER, Jerome A.
TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
FILE REFERENCE: 054094
CURRENT APPLICATION NUMBER: US/09/297,269
EARLIER FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: P03310
EARLIER FILING DATE: 1996-10-29
EARLIER APPLICATION NUMBER: P04306
EARLIER FILING DATE: 1996-12-19
EARLIER APPLICATION NUMBER: PCT/AU97/00721
EARLIER FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36
LENGTH: 41
TYPE: DNA
ORGANISM: synthetic construct
US-09-297-269-36

Query Match 48.7%; Score 14.6; DB 4; Length 41;
Best Local Similarity 81.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 ACCTGGCGAACAATGGTGAC 25
||||| ||| ||||| |||
Db 14 ACCTGGCGAAGCTGTGAC 34

RESULT 10

US-07-718-490-2/C
Sequence 2, Application US/07718490
Patent No. 5340716

GENERAL INFORMATION:
APPLICANT: Ullman, Edwin F.
APPLICANT: Kirakossian, Hrair
APPLICANT: Pease, John S.
APPLICANT: Daniloff, Yuri
APPLICANT: Wagner, Daniel B.
TITLE OF INVENTION: Assay Method Utilizing Photoactivated
TITLE OF INVENTION: Chemiluminescent Label
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syntex (U.S.A.) Inc.
STREET: 3401 Hillview Avenue
CITY: Palo Alto

STATE: California
COUNTRY: U.S.A.
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,490
FILING DATE: 19910620
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: Letterer, Theodore J.
REGISTRATION NUMBER: 28,319
REFERENCE/DOCKET NUMBER: 27340/ DO-1557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1091
TELEFAX: (415) 496-3529

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: NUCLEIC ACID

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: K12 DNAJ
INDIVIDUAL ISOLATE: Synthetic
US-07-718-490-2

Query Match 48.0%; Score 14.4; DB 1; Length 30;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 2 TCACCTGGCAGACATGTGAC 25
||| ||||| ||||| |||
Db 29 TGAAGCGGCGAGCATGCGCAC 6

RESULT 11

US-07-718-490-1
Sequence 1, Application US/07718490
Patent No. 5340716

GENERAL INFORMATION:
APPLICANT: Ullman, Edwin F.
APPLICANT: Kirakossian, Hrair
APPLICANT: Pease, John S.
APPLICANT: Daniloff, Yuri
APPLICANT: Wagner, Daniel B.
TITLE OF INVENTION: Assay Method Utilizing Photoactivated
TITLE OF INVENTION: Chemiluminescent Label
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syntex (U.S.A.) Inc.
STREET: 3401 Hillview Avenue
CITY: Palo Alto
STATE: California
COUNTRY: U.S.A.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,490
FILING DATE: 19910620
CLASSIFICATION: 436

```

ATTORNEY/AGENT INFORMATION:
NAME: Leitner, Theodore J.
REGISTRATION NUMBER: 28,319
REFERENCE/DOCKET NUMBER: 27340/ DO-1557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 852-1091
TELEFAX: (415) 496-3529
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)T
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
STRAIN: K12 DNAJ
INDIVIDUAL ISOLATE: Synthetic
US-07-718-490-1

Query Match      48.0%; Score 14.4; DB 1; Length 50:
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY      2 TCACCTGGCGAATGTCGACAC 25
Db      12 TGAACGGCGGACGATGCGGCAC 35

RESULT 12
US-08-471-496-7
Sequence 7, Application US/08471496
Patent No. 5798223
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,496
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/02645
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0830001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

```

```

MOLECULE TYPE: CDNA
US-08-471-496-7

Query Match      47.3%; Score 14.2; DB 1; Length 34:
Best Local Similarity 70.4%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY      3 CAACCTGGCGAATGTCGACCCCAT 29
Db      4 CAAGCTTGCACCATCTCGGCGCCAT 30

RESULT 13
US-08-894-840-7
Sequence 7, Application US/08894840
Patent No. 5859200
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: HUMAN AMINE TRANSPORTER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,840
FILING DATE: 29-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0830000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-894-840-7

Query Match      47.3%; Score 14.2; DB 2; Length 34:
Best Local Similarity 70.4%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY      3 CAACCTGGCGAATGTCGACCCCAT 29
Db      4 CAAGCTTGCACCATCTCGGCGCCAT 30

RESULT 14
US-09-139-675-7
Sequence 7, Application US/09139675A
Patent No. 6117426
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: ROSEN, CRAIG
TITLE OF INVENTION: Human Amine Transporter
FILE REFERENCE: 1488.0830003
CURRENT APPLICATION NUMBER: US/09/139,675A

```

```

: CURRENT FILING DATE: 1998-08-25
: EARLIER APPLICATION NUMBER: WO PCT/US95/02645
: EARLIER FILING DATE: 1995-03-01
: EARLIER APPLICATION NUMBER: US 08/471,496
: EARLIER FILING DATE: 1995-06-06
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 7
: LENGTH: 34
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-139-675-7

```

```

Query Match          47.3%: Score 14.2; DB 3: Length 34;
Best Local Similarity 70.4%: Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

QY      3 CAACCTGGCGACATGCTGAACCCCAT 29
        ||| ||| ||| ||| ||| ||| |||
Db      4 CAAGCTTGCACCATGCTGCGCCCAT 30

```

```

RESULT 15
US-08-853-774-11
: Sequence 11, Application US/08853774
: Patent No. 6265557
: GENERAL INFORMATION:
: APPLICANT: Diamond, David
: APPLICANT: Nehlsen-Cannarella, Sandra
: APPLICANT: Fagoaga, Omar
: APPLICANT: Szalay, Aladar
: TITLE OF INVENTION: ABO HISTO-BLOOD GROUP O ALLELES OF THE BABOON
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobb, Martens, Olson & Bear
: STREET: 620 Newport Center Drive Sixteenth Flo
: CITY: Newport Beach
: STATE: CA
: COUNTRY: USA
: ZIP: 92660
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/853,774
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Altman, Daniel E.
: REGISTRATION NUMBER: 34,115
: REFERENCE/DOCKET NUMBER: LOMAIMM.100A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 714/760-0404
: TELEFAX: 714/760-9503
: TELEX:
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-853-774-11

```

```

Query Match          46.7%: Score 14; DB 4: Length 28;
Best Local Similarity 77.3%: Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY 8 TGGCGAACATGCTGAACCCCAT 29

```

Db      5 TGGCAACACAGTTAACCACAT 26

```

Search completed: June 22, 2003, 00:01:32
Job time : 36.625 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 88.5938 Seconds
(without alignments)
496.907 Million cell updates/sec

Title: US-09-964-666-11

Perfect score: 30

Sequence: 1 ATCAACCTGGCGACATGCTGAACCCCATC 30

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Published Applications_NA.*
2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	30	100.0	30	9	US-09-964-667-11
2	30	100.0	30	10	US-09-964-666-11
3	30	100.0	30	10	US-09-964-412-11
4	19	63.3	49	9	US-09-860-670-233
5	16.8	56.0	30	9	US-10-085-906-77
6	16.6	55.3	29	9	US-09-530-139-69
7	16.2	54.0	22	9	US-09-530-139-70
8	16.2	54.0	24	10	US-09-885-441-35
9	16	53.3	32	9	US-10-123-170-17
10	15.2	50.7	20	10	US-09-752-983-259
11	15.2	50.7	20	10	US-09-800-631-32
12	15.2	50.7	31	10	US-09-801-274-1110
13	15.2	50.7	36	9	US-09-877-478-6391
14	15.2	50.7	37	9	US-09-877-478-4044
15	15	50.0	25	9	US-10-098-2638-8701
16	15	50.0	41	9	US-10-239-804-23
17	15	50.0	41	9	US-10-239-804-36
18	14.8	49.3	20	9	US-09-771-933-148
19	14.6	48.7	26	10	US-09-740-668A-55

20	14.6	48.7	30	9	US-10-085-906-241	Sequence 241, App
21	14.4	48.0	37	10	US-09-755-665-108	Sequence 108, App
22	14.2	47.3	30	10	US-09-964-277-15	Sequence 15, App
23	14.2	47.3	31	9	US-09-924-125-4	Sequence 4, App
24	14.2	47.3	34	10	US-09-987-025-12	Sequence 12, App
25	14.2	47.3	37	9	US-09-780-533A-4302	Sequence 4302, App
26	14.2	47.3	37	9	US-09-780-533B-4387	Sequence 4387, App
27	14.2	47.3	37	9	US-09-877-478-4122	Sequence 4122, App
28	14.2	47.3	37	9	US-09-930-423-2915	Sequence 2915, App
29	14	46.7	24	9	US-09-940-185-2688	Sequence 2688, App
30	14	46.7	25	9	US-10-098-2638-25783	Sequence 25783, App
31	14	46.7	30	9	US-09-832-292-24	Sequence 24, App
32	13.8	46.0	20	9	US-10-025-201-13	Sequence 13, App
33	13.8	46.0	25	9	US-10-192-926-18	Sequence 18, App
34	13.8	46.0	37	9	US-09-930-423-2785	Sequence 2785, App
35	13.8	46.0	37	9	US-09-930-423-2860	Sequence 2860, App
36	13.8	46.0	46	9	US-10-146-938-1	Sequence 1, App
37	13.6	45.3	20	9	US-10-085-906-365	Sequence 365, App
38	13.6	45.3	23	10	US-09-529-063-86	Sequence 86, App
39	13.6	45.3	30	9	US-10-085-906-44	Sequence 44, App
40	13.6	45.3	30	9	US-09-864-636A-1614	Sequence 1614, App
41	13.6	45.3	31	10	US-09-801-274-1365	Sequence 1365, App
42	13.6	45.3	33	9	US-10-155-233-10	Sequence 10, App
43	13.6	45.3	37	9	US-09-730-289B-2710	Sequence 2710, App
44	13.6	45.3	37	9	US-09-780-533A-4376	Sequence 4376, App
45	13.6	45.3	37	9	US-09-877-478-4115	Sequence 4115, App

ALIGNMENTS

RESULT 1
US-09-964-667-11
Sequence 11, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Wands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-667-11

Query Match 100.0%; Score 30; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACATGCTGAACCCCATC 30
1 ATCAACCTGGCGAACATGCTGAACCCCATC 30

RESULT 2

US-09-964-666-11
Sequence 11, Application US/09964666
Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-666-11

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACATGCTGAACCCCATC 30
1 ATCAACCTGGCGAACATGCTGAACCCCATC 30

RESULT 3

US-09-964-412-11
Sequence 11, Application US/09964412
Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-964-412-11

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACATGCTGAACCCCATC 30
1 ATCAACCTGGCGAACATGCTGAACCCCATC 30

RESULT 4

US-09-860-670-233
Sequence 233, Application US/09860670
Patent No. US20020165137A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA127P1

CURRENT APPLICATION NUMBER: US/09/860,670

CURRENT FILING DATE: 2001-05-21

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 289

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 233

LENGTH: 49

TYPE: DNA

ORGANISM: Homo sapiens

US-09-860-670-233

Query Match 63.3%; Score 19; DB 9; Length 49;
Best Local Similarity 81.5%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACATGCTGAACCCCATC 27
1 ATCAACCTGGCGAACATGCTGAACCCCATC 27

RESULT 5

```

US-10-085-906-77/c
: Sequence 77, Application US/10085906
: Publication No. US20030054371A1
: GENERAL INFORMATION:
: APPLICANT: Ying, Vincent
: APPLICANT: Wu, Paul
: APPLICANT: Gray, Gary S.
: TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
: FILE REFERENCE: GNN-5143CP2
: CURRENT APPLICATION NUMBER: US/10/085, 906
: CURRENT FILING DATE: 2002-02-27
: PRIOR APPLICATION NUMBER: US 60/126,215
: PRIOR FILING DATE: 1999-03-25
: PRIOR APPLICATION NUMBER: US 09/534,061
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: PCT/US00/07938
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 545
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 77
: LENGTH: 30
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-085-906-77

```

	Query Match	56.0%	Score 16.8;	DB 9;	length 30;
	Best Local Similarity	90.0%	Pred. NO.3,7e+02;		
	Matches	18; Conservative	0; Mismatches	2; Indels	Gaps 0.
OY	8 TGGCGAACATGCTGAACCC	27			
Db	30 TGGCGAACATGCTGAACCC	11			

```

RESULT 6
US-09-530-139-69/C
: Sequence 69, Application US/09530139
: Publication No. US20030092852A1
: GENERAL INFORMATION:
: APPLICANT: FRENKEN, LEON GERARDUS
: APPLICANT: HOWELL, STEVEN
: APPLICANT: LEDERBOER, ADRIANUS MARINUS
: APPLICANT: VAN DER LOGT, CORNELIS PAUL
: TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
: FILE REFERENCE: 60113/268075/ASH
: CURRENT APPLICATION NUMBER: 05/09/530,139
: CURRENT FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: PCT/EP98/06991
: PRIOR FILING DATE: 1998-10-27
: PRIOR APPLICATION NUMBER: EP 97308538.4
: PRIOR FILING DATE: 1997-10-27
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 69
: LENGTH: 29
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
: US-09-530-139-69

```

Query Match	55.3%	Score 16.6	DB 9	Length 29
Best Local Similarity	82.6%	Pred. No. 4.5e+02		
Matches 19, Conservative	0	Mismatches 4	Indels 0	Gaps 0
OY	5	ACTGCGCAACATGCTGAACCC	27	
db	26	ACCTGTGGAACCTGTGAGAACAC	4	

RESULT 7
US-09-530-139-70

```

Sequence 70. Application US/09530139
: Publication NO. US20030092862A1
:
: GENERAL INFORMATION:
: APPLICANT: FRENKEN, LEON GERARDUS
: APPLICANT: HOWELL, STEVEN
: APPLICANT: LEDERBOER, ADRIANUS MARINUS
: APPLICANT: VAN DER LOGT, CORNELIS PAUL
: TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
: FILE REFERENCE: 60113/268075/ASH
: CURRENT APPLICATION NUMBER: US/09/530,139
: CURRENT FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: PCT/EP98/06991
: PRIOR FILING DATE: 1998-10-27
: PRIOR APPLICATION NUMBER: EP 97308538.4
: PRIOR FILING DATE: 1997-10-27
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 70
:
: LENGTH: 22
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
: US-09-530-139-70

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Query Match	54.0%;	Score 16.2;	DB 9;	Length 22;
Best Local Similarity	85.7%;	Pred. No. 6.5e+02;		
Matches	18;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
OY	5	ACCTGGCGACATGCTGAACC	25	
	1	ACCTGGTGAACATGCTGAACC	21	

```

RESULT 8
US-09-885-441--35/c
: Sequence 35. Application US/09885441
: Patent No. US20020146407A1
: GENERAL INFORMATION:
: APPLICANT: XIAO, Yonghong
: TITLE OF INVENTION: Regulation of Human Eosinophil Serine
: PROTEIN: Proteinase-1-Like Enzyme
: FILE REFERENCE: 04974.00512
: CURRENT APPLICATION NUMBER: US/09/885,441
: CURRENT FILING DATE: 2001-06-21
: PRIOR APPLICATION NUMBER: US 60/212,844
: PRIOR FILING DATE: 2000-06-21
: PRIOR APPLICATION NUMBER: US 60/244,171
: PRIOR FILING DATE: 2000-10-31
: PRIOR APPLICATION NUMBER: US 60/279,766
: PRIOR FILING DATE: 2001-03-30
: PRIOR APPLICATION NUMBER: PCT/____
: PRIOR FILING DATE: 2001-06-20
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 35
: LENGTH: 24
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-885-441--35

```

Query Match	54.0%;	Score 16.2;	DB 10;	Length 24;
Best Local Similarity	85.7%;	Pred. No. 6	5e2;	
Matches	18;	Conservative	0;	Mismatches 3;
				Indels 0;
				Gaps 0;
QY	7	CTGGCGAACATGTGAACCC	27	
Db	24	CTGGTCAACACAGGTGAACCC	4	

RESULT 9
US-10-123-170-17
; Sequence 17, Application US/10123170

Publication No. US2003008277A1
GENERAL INFORMATION:
APPLICANT: ESCRIOU, NICOLAS
APPLICANT: VAN DER WERF, SYLVIE
APPLICANT: VIEIRA-MACHADO, ALEXANDRE
APPLICANT: VIEIRA-MACHADO, ALEXANDRE
TITLE OF INVENTION: RECOMBINANT SEGMENTED NEGATIVE STRAND VIRUS CONTAINING BICISTRONIC
TITLE OF INVENTION: SEGMENT WITH A DUPLICATION OF ITS 3' NONCODING FLANKING SEQUENCE
TITLE OF INVENTION: AND THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
FILE REFERENCE: 221283US0
CURRENT APPLICATION NUMBER: US/10/123,170
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/283,957
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 17
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic DNA
US:10-123-170-17

Query Match 53.3%; Score 16; DB 9; Length 32;
Best Local Similarity 79.2%; Pred. No. 8.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 ACCTGGGACATGCTGAACCCCA 28
DB 2 ACCTCGAGACATGAGAGACATCA 25

RESULT 10
US-09-752-983-259
Sequence 259, Application US/09/52983
Patent No. US20010016575A1

GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia

TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.
ZIP: 08053

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,983
FILING DATE: 02-Jan-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/280,805
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454

INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid

STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-09-752-983-259

Query Match 50.7%; Score 15.2; DB 10; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 8 TGGCGACATGCTGAACCC 27
DB 1 TGGCTAACACGCTGAACCC 20

RESULT 11
US-09-800-631-32/c
Sequence 32, Application US/09800631
Patent No. US2002008228A1

GENERAL INFORMATION:
APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST E
FILE REFERENCE: ISPH-0544
CURRENT APPLICATION NUMBER: US/09/800,631
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US/09/657,346
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 175
SEQ ID NO 32
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-800-631-32

Query Match 50.7%; Score 15.2; DB 10; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 7 CTGCGACATGCTGAACCC 26
DB 20 CTGACCAACATGCTGAACCC 1

RESULT 12
US-09-801-274-1110/c
Sequence 1110, Application US/09801274
Patent No. US20020032319A1

GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1110
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-1110

Query Match 50.7%; Score 15.2; DB 10; Length 31;
Best Local Similarity 77.3%; Pred. No. 1.8e+03;
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Mon Jun 23 10:01:49 2003

us-09-964-666-11.Length_Limit__50.rnpb

Page 6

Db ||||| | ||||| ||| |||
2 TCAACSTCGGGAACACGCTCAAC 24

Search completed: June 22, 2003, 03:18:19
Job time : 91.5938 secs

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BASE COUNT		7 a 7 c 15 g 21 t
ORIGIN		
Query Match	72.0%;	Score 21.6; DB 9; Length 50;
Best Local Similarity	85.7%;	Pred. No. 75;
Matches	24; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	1 ATCAACCTGGCGAACATGCTGAACCCCA 28 1	
Db	46 ACCAGCCTGGCGAACATGCTGAACCCA 19	
RESULT 2		
AUI06806/c	AUI06806	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AUI06806 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone	
DEFINITION	LNC05691, mRNA sequence.	
ACCESSION	AUI06806	
VERSION	AUI06806.1 GI:13556327	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 50)	
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hataza, 'H., Oda,I., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki, 'Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001) 21270072	
JOURNAL	Contact: Yutaka Suzuki	
MEDLINE	Department of Virology	
COMMENT	Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. 'S. Construction and Characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997). Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"	
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BASE COUNT	14 a 10 c 12 g 14 t	
ORIGIN		
Query Match	70.7%;	Score 21.2; DB 9; Length 50;
Best Local Similarity	88.5%;	Pred. No. 118+02;
Matches	23; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
OY	1 ATCAACCTGGCGAACATGCTGAACCC 26 	
Db	42 ATCAACCTGGCGAACATGCTGAACCC 17	
RESULT 3		
N80349/c	N80349	33 bp mRNA linear EST 02-APR-1996
LOCUS	zai3c12.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone	
DEFINITION	IMAGE:292438 5' similar to gb U13704 HUMSCALUB Human scRNA molecule , transcribed from Alu (rRNA); gb:X53795_rnal INDUCIBLE MEMBRANE	

ACCESSION	N80349
VERSION	N80349.1
KEYWORDS	GI:1243050
SOURCE	EST.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman M., Hultman,M., Kuwabara,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston R., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact: Wilton RK Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: reverse ER High quality sequence stop: 1. Location/Qualifiers 1..33 /organism="Homo sapiens" /db_xref="GDB:3800215" /db_xref="taxon:9606" /clone="IMAGE:292438" /clone_1lb="Soares fetal liver spleen INFLS" /sex="male" /dev_stage="20 week-post conception fetus" /lab_host="DH10B (ampicillin resistant)" /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site_1: Pac I - oligo(dT) primer: 1st strand cDNA was primed with a Pac I - oligo(dT) primer: [5' AACTGGAGAATTAATTAAAGATCTTTTGTTTTTTTTTTTT 3'] , double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT	7 a 6 c 7 t 2 others
ORIGIN	
Query Match	69.3%; Score 20.8; DB 14; Length 33;
Best Local Similarity	88.0%; Pred. No. 1.4e+02;
Matches	22: Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	3 CAACCTGGCGCAATGGAACCCC 27
Ddb	 33 CATCCTGGCTAACAATGCTGAANCC 9
RESULT 4	
AUI02526/c	50 bp mRNA linear EST 30-AUG-2001
LOCUS	AUI02526 Sugano Homo sapiens cdna library Homo sapiens CDNA clone
DEFINITION	COLF1341, mRNA sequence.
ACCESSION	AUI02526
VERSION	AUI02526.1 GI:13552046
KEYWORDS	EST.
SOURCE	human. Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 50)
AUTHORS	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake, H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki, Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maryama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="COLF1341"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT 9 a 9 c 17 g 15 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 9; Length 50;
Best Local Similarity 85.2%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTCGAACCCC 27
1 ||| ||||| ||||| ||||| |||
43 ACCAGCCTGGCCACAATGTCGAACCCC 17

Db

RESULT 5
AU105702 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU105702 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC11393, mRNA sequence.
ACCESSION AU105702
VERSION AU105702.1 GI:13555223
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, F., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maryama, K., Suyama, A. and Sugano, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC11393"
/clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumarate treated U937 cells"

BASE COUNT 13 a 16 c 12 g 9 t

ORIGIN

Query Match 68.7%; Score 20.6; DB 9; Length 50;
Best Local Similarity 85.2%; Pred. No. 1.9e+02;

Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTCGAACCCC 27
1 ||| ||||| ||||| ||||| |||
14 ACCAGCCTGGCCACAATGTCGAACCCC 40

Db

RESULT 6
AA492220 44 bp mRNA linear EST 19-AUG-1997
LOCUS AA492220
DEFINITION ng79604.s1 NCI-CGAP-P6 Homo sapiens cDNA clone IMAGE:940974 similar to gb:M91159.1111 ALU CLASS E WARNING ENTRY !!!!! (HUMAN); mRNA sequence.
AA492220
AA492220.1 GI:2221782
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 44)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.101.gov/bdrp/image/image.html
Insert length: 575 Std Error: 0.00
Seq primer: 40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 44
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/db_xref="taxon:9606"
/clone="IMAGE:940974"
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/sex="male"
/tissue_type="prostate"
/lab_host="DH10B"
/note="Vector: pAMP10; mRNA made from prostatic intraepithelial neoplasia (low-grade), cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp.. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

BASE COUNT 15 a 14 c 7 g 8 t

ORIGIN

Query Match 68.0%; Score 20.4; DB 9; Length 44;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATCAACCTGGCGAACAATGTCGAACCCATC 30
1 ||| ||||| ||||| ||||| |||
3 ACCAGCCTGGCCACAATGTCGAACCCACC 32

Db

RESULT 7
AU103189 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU103189 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC04023, mRNA sequence.
ACCESSION AU103189
VERSION AU103189.1 GI:13552710
KEYWORDS EST.

SOURCE ORGANISM human.
SOURCE HOMO sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Oka,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.
S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
SOURCE Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC04023"
/clone_jdb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylflumate treated u937 cells"
BASE COUNT 9 a 7 c 15 g 19 t
ORIGIN
Query Match 67.3%; Score 20.2; DB 9; Length 50;
Beet Local Similarity 88.0%; Pred.No.2.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CACCTGGCGACATGCTGTAACCC 27
|| ||||| ||||| ||||| ||||
49 CAGCTGGCCAACTGCTGAACCC 25
Db
RESULT 8
LOCUS T53436 33 bp mRNA linear EST 06-FEB-1995
DEFINITION ya89a10.s1 Stragene placenta (937225) Homo sapiens cDNA clone IMAGE:68826.3', similar to similar to gb:W87338 ACTIVATOR 1 40 KD
ACCESSION T53436
VERSION T53436
KEYWORDS T53436.1 GI:655296
EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chisoe,S., Dietrich,N., Dubugue,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Treviski,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
TITLE Generation and analysis of 280,000 human expressed sequence tags
JOURNAL Genome Res. 6 (9), 807-828 (1996)
MEDLINE 97044478
COMMENT Other_ESTs: ya89a10.r1
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNC

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Three considered overall poor quality
 Seq primer: -21m13
 High quality sequence stop: 1.

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        /db_xref="taxon:9606"
        /clone="IMAGE:68826"
        /clone_lib="Stratagene placenta (#937225)"
        /sex="male"
        /lab_host="SOUR cells (kanamycin resistant)"
        /note="Organ: placenta; Vector: pluscript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Caucasian. Average insert size: 1.2 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGGAG 3' -3' adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTTTTT 3'"
BASE COUNT      10 a       12 c       7 g       4 t
ORIGIN
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Best Local Similarity 81.5%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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         1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      7 ACCAGCCTGCACCACATCGGGAACCCC 33

RESULT 9
LOCUS          AU102524/c                    50 bp   mRNA   linear   EST 30-AUG-2001
DEFINITION     AU102524 Suguano Homo sapiens cDNA library Homo sapiens CDNA clone
               COI.07268, mRNA sequence.
ACCESSION      AU102524
VERSION        AU102524.1 GI:13552044
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 50)
AUTHORS       Suzuki,Y., Tsai,H., Tsunoda,T., Mizushima-Sugano,J., Seze,J., Hatake,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
               Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
               EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL       21270072
MEDLINE
COMMENT       Contact: Yutaka Suzuki
               Department of Virology
               Institute of Medical Science, University of Tokyo
               4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
               Email: yusuzuki@ims.u-tokyo.ac.jp
               Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S.
               Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
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BASE COUNT      10 a       12 c       12 g       16 t
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Query Match     63.3%; Score 19; DB 9; Length 50;
Best Local Similarity 81.5%; Pred. No. 8.3e+02;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy	1	ATCAACCTGGCGACATGTCGTAACCC	27	
Db	39	ACCAAGCTGCGCAACATGTCGTAAC	13	
RESULT 10				
AU102525/c				
LOCUS				
DEFINITION	AU102525	Sugano Homo sapiens	cdNA library	Homo sapiens
ACCESSION	AU102525			
VERSION	AU102525.1	GI:13552045		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 50)			
	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata			
	,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki			
	,Y., Nakamura,Y., Suyama,A. and Sugano,S.			
	Diverse transcriptional Initiation revealed by fine, large-scale			
	mapping of mRNA start sites			
	EMBO Rep. 2 (5), 388-393 (2001)			
	21270072			
JOURNAL	Contact: Yutaka Suzuki			
MEDLINE	Institute of Medical Science, University of Tokyo			
COMMENT	Department of Medical Science, University of Tokyo			
	4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan			
	Email: yusuzuki@ims.u-tokyo.ac.jp			
	Suzuki,Y., Yoshimoto-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano			
	,S. Construction and characterization of a full length-enriched and			
	a 5'-end-enriched cdNA library. Gene 200 (1-2), 149-156 (1997).			
FEATURES	Location/Qualifiers			
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Db	41	ACCAAGCTGCGCAACATGTCGTAAC	15	
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LOCUS				
DEFINITION	AU102525	Sugano Homo sapiens	cdNA library	Homo sapiens
ACCESSION	AU102525			
VERSION	AU102525.1	GI:13552049		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 50)			
	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata			
	,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki			
	,Y., Nakamura,Y., Suyama,A. and Sugano,S.			
	Diverse transcriptional Initiation revealed by fine, large-scale			
	mapping of mRNA start sites			
	EMBO Rep. 2 (5), 388-393 (2001)			
JOURNAL				

```

FEATURES
    source
        Contact: Yutaka Suzuki
        Department of Virology
        Institute of Medical Science, University of Tokyo
        4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
        Email: yszuki@ims.u-tokyo.ac.jp
        Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY
1 ATCAACCTGGCGAACAATGTTGAACCC 27
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LOCUS           AU102530 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      HS102245, mRNA sequence.
ACCESSION       AU102530
VERSION         AU102530.1 GI:13552050
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE       1 (bases 1 to 50)
AUTHORS        Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
               ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
               Diverse transcriptional initiation revealed by fine, large-scale
               mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE           Contact: Yutaka Suzuki
JOURNAL         Department of Virology
MEDLINE         Institute of Medical Science, University of Tokyo
                 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                 Email: yszuki@ims.u-tokyo.ac.jp
                 Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and
                 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
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Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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ACCESSION	NBLAN362NF		mRNA sequence.
VERSION	AU102535		
KEYWORDS	AU102535.1 GI:13552056		EST.
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 50)		
JOURNAL	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake		
MEDLINE	,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki		
COMMENT	,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001) 21270072		
FEATURES	Source		
ORIGIN	1..50		
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Query Match	63.3%	Score 19;	DB 9; Length 50;
Best Local Similarity	81.5%;	Pred. No. 8.3e+02;	
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DEFINITION	AU102667 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone		
ACCESSION	AKDA03070		mRNA sequence.
VERSION	AU102667		
KEYWORDS	AU102667.1 GI:13552188		EST.
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 50)		
JOURNAL	Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hatake		
MEDLINE	,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki		
COMMENT	,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001) 21270072		
CONTACT	Yutaka Suzuki		

	FEATURES	SOURCE	Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Suganoc, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
	LOCATION/Qualifiers	1..50	
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	Best Local Similarity	81.5%;	Pred. No. 8.3e+02;
	Matches	22; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
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	I I I I I I I I I I I I I I I I I I		
Dd	29 ACCAGCCTTGCCCAATATGTGTGAATCCC	3	
	RESULT 15	50 bp mRNA linear EST 30-AUG-2001	
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	LOCUS AU103194/c		
	DEFINITION AU103194 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone		
	NBLAN2977NF, mRNA sequence.		
	ACCESSION AU103194		
	VERSION AU103194.1 GI:13552715		
	KEYWORDS EST.		
	SOURCE human.		
	ORGANISM Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 50) Suzuki,Y., Talra,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hattara ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki ,Y., Nakamura,Y., Suyama,A. and Sugano,S. Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites EMBO Rep. 2 (5), 388-393 (2001)		
	CONTACT: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Suganoc, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).		
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	1..50		
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	Best Local Similarity	81.5%;	Pred. No. 8.3e+02;
	Matches	22; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
OY	1 ATCAACCTGGCGAACAATGTTGAACCCC	27	
	I I I I I I I I I I I I I I I I I I		
Dd	47 ACCAGCCTTGCACCAATGTTGAACCCC	21	

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Job time : 1299.03 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds
(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-12
Perfect score: 14
Sequence: 1 CACTGCACTTCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Geneml :
1: gb_ba :
2: gb_htg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sts :
12: gb_sy :
13: gb_un :
14: gb_vi :
15: em_ba :
16: em_fun :
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26: em_ro :
27: em_sts :
28: em_un :
29: em_vi :
30: em_htg_hum :
31: em_htg_inv :
32: em_htg_other :
33: em_htg_mus :
34: em_htg_pln :
35: em_htg_rod :
36: em_htg_mam :
37: em_htg_vrt :
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39: em_hgo_hum :
40: em_hgo_mus :
41: em_hgo_other :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	13	92.9	25	6	AR071993
2	12	85.7	27	6	I06372
3	11.4	81.4	20	6	AR193144
4	11.4	81.4	31	6	AR154129
5	11.4	81.4	36	6	AR077368
6	11.4	81.4	36	6	AR077405
7	11.4	81.4	36	6	AR117988
8	11.4	81.4	36	6	I95709
9	11	78.6	20	6	AX294160
10	11	78.6	20	6	AX296756
11	11	78.6	24	6	AX289527
12	11	78.6	24	6	AX292123
13	11	78.6	47	6	AX378274
14	10.4	74.3	18	6	AR049979
15	10.4	74.3	18	6	AR182515
16	10.4	74.3	20	6	AR158847
17	10.4	74.3	20	6	AR158848
18	10.4	74.3	20	6	AR158849
19	10.4	74.3	20	6	AR158850
20	10.4	74.3	20	6	AR158851
21	10.4	74.3	20	6	AR158852
22	10.4	74.3	20	6	AR158853
23	10.4	74.3	20	6	AR158854
24	10.4	74.3	20	6	AR173023
25	10.4	74.3	21	6	AR000120
26	10.4	74.3	21	6	AR205963
27	10.4	74.3	22	6	AR083596
28	10.4	74.3	22	6	AR110255
29	10.4	74.3	22	6	AX467734
30	10.4	74.3	25	6	AX042456
31	10.4	74.3	29	6	BD013007
32	10.4	74.3	29	23	BD010040
33	10.4	74.3	30	7	PEDRFGMBY
34	10.4	74.3	36	6	A07187
35	10.4	74.3	36	6	E59618
36	10.4	74.3	36	6	I05106
37	10.4	74.3	36	6	I07406
38	10.4	74.3	36	6	I07637
39	10.4	74.3	36	6	I71445
40	10.4	74.3	41	6	AR077392
41	10.4	74.3	41	6	AR077493
42	10.4	74.3	41	6	AR118012
43	10.4	74.3	41	6	I95733
44	10.4	74.3	44	6	AR077636
45	10.4	74.3	45	6	AX201429

ALIGNMENTS

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LOCUS AR071993/c 25 bp DNA
DEFINITION Sequence 23 from patent US 5912168.
ACCESSION AR071993
VERSION AR071993.1 GI:7222881
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Watson,J.D. and Ruder,T.F.
TITLE CD95 regulatory gene sequences
JOURNAL Patent: US 5912168-A 23 15-JUN-1999;
FEATURES Location/Qualifiers

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OY: 1 CACTGCACCTTNCCA 14
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Db 23 CACTGCACCTTACCA 10

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LOCUS 106372
DEFINITION Sequence 33 from Patent EP 0293934.
ACCESSION 106372
VERSION 106372.1 GI:590632
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)
AUTHORS Mulvihill, E.R., Nexo, B.A., Yoshitake, S., Ikeda, Y., Suzuki, S.,
Hashimoto, A. and Yuzuriha, T.
TITLE Mutant t-PA with kringles replacement
JOURNAL Patent: EP 0293934-A1 33 07-DEC-1988;
FEATURES Location/Qualifiers
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/organism="unknown"

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ORIGIN

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OY: 1 CACTGCACCTTNCC 13
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DEFINITION Sequence 29 from patent US 6346416.
ACCESSION AR193144
VERSION AR193144.1 GI:20239109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dean, N.M. and Cowse, L.M.
TITLE Antisense inhibition of HPK/GCK-like kinase expression
JOURNAL Patent: US 6346416-A 29 12-FEB-2002;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"

BASE COUNT 3 a 7 c 4 g 6 t
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCCA 14
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Db 1 CACTGCACCTTCCA 14

RESULT 4
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DEFINITION Sequence 7 from patent US 6238866.
ACCESSION AR154129
VERSION AR154129.1 GI:15122182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 31)
AUTHORS Yeh, H.R. and Wlick, C.H.
TITLE Detector for nucleic acid typing and methods of using the same
JOURNAL Patent: US 6238866-A 7 29-MAY-2001;
FEATURES Location/Qualifiers
source 1. .31
/organism="unknown"

BASE COUNT 7 a 14 c 3 g 7 t
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 1.9e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY: 1 CACTGCACCTTNCCA 14
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Db 9 CACTGCACCTTCCA 22

RESULT 5
LOCUS AR077368
DEFINITION Sequence 83 from patent US 5962255.
ACCESSION AR077368
VERSION AR077368.1 GI:10004114
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 36)
AUTHORS Griffiths, A. David., Williams, S. Cameron., Waterhouse, P. Michael.,
Nissim, A., Winter, G. Paul., Johnson, K. Stuart. and
Smith, A. John. Hammond.
TITLE Methods for producing recombinant vectors
JOURNAL Patent: US 5962255-A 83 05-OCT-1999;
FEATURES Location/Qualifiers
source 1. .36
/organism="unknown"

BASE COUNT 10 a 13 c 7 g 6 t
ORIGIN

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Best Local Similarity 85.7%; Pred. No. 1.9e+04;
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OY: 1 CACTGCACCTTNCCA 14
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Db 9 CACTGCACCTTGCCA 22

RESULT 6
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DEFINITION Sequence 120 from patent US 5962255.
ACCESSION AR077405
VERSION AR077405.1 GI:10004151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 36)
AUTHORS Griffiths, A. David., Williams, S. Cameron., Waterhouse, P. Michael.,
Nissim, A., Winter, G. Paul., Johnson, K. Stuart. and

TITLE	Smith, A. John. Hammond.
JOURNAL	Methods for producing recombinant vectors
FEATURES	Patent: US 5962255-A 120 05-OCT-1999;
	Location/Qualifiers

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ORIGIN	/organism="unknown"		

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Best Local Similarity	85.7%	Pred. No. 1.9e+04		
Matches 12; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY	1	C	A	C	T	G	C	A	C	T	T	N	C	C	A	14
Db	9	C	A	G	T	G	C	A	C	T	T	G	C	C	A	22

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	FEATURES
AR117988	AR117988	Sequence 37 from patent US 6140471.	AR117988	AR117988.1	GI:14098094

SOURCE ORGANISM

REFERENCE	1 (bases 1 to 36)
AUTHORS	Johnson, K. Start., Winter, G. Paul., Griffiths, A. David., Smith, A. John, Hammond, and Waterhouse, P. Michel.
TITLE	Methods for producing members of specific binding pairs
JOURNAL	Patent: US 6140471-A 37 31-Oct-2000;
FEATURES	Location/Qualifiers
source	1 36

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Matches	12	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

OY	1 CACTGCACCTNCCA	14
Db	9 CAGTGCACCTTGCCA	22

RESULT 8			
LOCUS	195709	36 bp	DNA
DEFINITION	Sequence 37 from patent US 5733743.	Linear	PAT 01-DEC-1998

VERSION	195709.1	GI:3940179
KEYWORDS	.	
SOURCE	Unknown.	

REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 36) Johnson, K. Stuart., Gibbs, J. H. "

TITLE	JOURNAL	FEATURES
Methods for producing members of specific binding pairs	Patent: US 5733743-A 37 31-MAR-1998;	Location/Qualifiers

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BASE COUNT      /organism="unknown"
ORIGIN          10 a          13 c          7 g          6 t

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Query Match	81.4%	Score 11.4	DB 6	Length 36
Best Local Similarity	85.7%	Score No. 1.9e+04		
Matches 12	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	1	CACTGCACCTNCCA	14
Db	9	CAGTGCACCTTGCCA	22

	20 bp	DNA	linear	PAT 21-NOV-2001
RESULT 9				
AX294160/c				
LOCUS				
AX294160				

ACCESSION	AX294160
VERSION	AX294160.1
KEYWORDS	GI:17055843

ORGANISM	synthetic construct artificial sequences.
REFERENCE	1

AUTHORS	Barany, F., Zivri, M., Gerry, N. P., Favis, R. and Kliman, R.
TITLE	Method of designing addressable array for detection of nucleic acid
JOURNAL	Sequence differences using ligase detection reaction
Patent:	WO 0179548-A 5922 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)	
Location/Qualifiers	
FEATURES	

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT      5 a      6 c      7 g      2 t
ORIGIN

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Best Local Similarity	91.7%	Pred. No.	3.5e+04	
Matches 11	Conservative	0	Mismatches 1	Indels 0
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QY	3	CTGCACCTTNGCA	14
Db	18	CTGCACCTTGCCA	7

RESULT 10			
AX296756/c			
LOCUS	AX296756	20 bp	DNA
DEFINITION	Sequence 8518 from Patent WO0179548.	Linear	PAT 21-NOV-2001

SOURCE	synthetic construct.
ORGANISM	synthetic construct

artificial sequences.

AUTHORS	TITLE
Barany, F., Zilry, M., Gerry, N.P., Favis, R. and Kliman, R.	Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction

CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT      4 a      4 c      8 g      4 t

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Query Match	78.6%;	Score 11;	DB 6;	Length 20;
Best Local Similarity	91.7%;	Pred. No. 3.5e+04;		

QY . 1 CACTGCACTTNC 12
| | | | | | | | | |
|

RESULT 11
AX289527/C

LOCUS AX289527 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 1289 from Patent WO0179548.
ACCESSION AX289527
VERSION AX289527.1 GI:17051210
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 1289 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 6 a 8 c 7 g 3 t
ORIGIN
Query Match 78.6%; Score 11; DB 6; Length 24;
Best Local Similarity 91.7%; Pred. NO. 3.5e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 CTGCACCTNCCA 14
Db 22 CTGCACCTGCCA 11
RESULT 12
LOCUS AX292123 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 3885 from Patent WO0179548.
ACCESSION AX292123
VERSION AX292123.1 GI:17053806
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
PATENT: WO 0179548-A 3885 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
BASE COUNT 4 a 7 c 8 g 5 t
ORIGIN
Query Match 78.6%; Score 11; DB 6; Length 24;
Best Local Similarity 91.7%; Pred. NO. 3.5e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CACTGCACCTNC 12
Db 16 CACTGCACCTGC 5
RESULT 13
LOCUS AX378274 47 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 63 from Patent WO0206525.
ACCESSION AX378274
VERSION AX378274.1 GI:19574124
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
TITLE Obesity associated diallelic marker maps
JOURNAL Patent: WO 0206525-A 63 24-JAN-2002;
GENSET (FR)
FEATURES
source 1..47
/organism="Homo sapiens"
/db_xref="taxon:9606"
variation 24
/note="99-28363-114 : polymorphic base A or G"
BASE COUNT 9 a 8 c 15 g 14 t 1 others
ORIGIN
Query Match 78.6%; Score 11; DB 6; Length 47;
Best Local Similarity 78.6%; Pred. NO. 3.6e+04;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 CACTGCACCTNCCA 14
Db 32 CACTGCACCTGCCA 19
RESULT 14
LOCUS AR049979 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5824794.
ACCESSION AR049979
VERSION AR049979.1 GI:5971971
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Borden,P.Ann. and Heller,R.Anand.
TITLE Human stromelysin-1 promoter
JOURNAL Patent: US 5824794-A 2 20-OCT-1998;
FEATURES
source 1..18
/organism="unknown"
BASE COUNT 2 a 9 c 1 g 6 t
ORIGIN
Query Match 74.3%; Score 10.4; DB 6; Length 18;
Best Local Similarity 84.6%; Pred. NO. 8.9e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CACTGCACCTNCC 13
Db 3 CACTGCCTTACC 15
RESULT 15
LOCUS AR182515 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6338944.
ACCESSION AR182515
VERSION AR182515.1 GI:20225722
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Borden,P.Ann. and Heller,R.Anand.
TITLE Methods for measuring stromelysin-1 promoter activity
JOURNAL Patent: US 6338944-A 2 15-JAN-2002;
FEATURES
source 1..18
/organism="unknown"
BASE COUNT 2 a 9 c 1 g 6 t
ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 18;
 Best Local Similarity 84.6%; Pred. No. 8.9e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CACTGCACTTNC 13
 ||||| |||
 Db 3 CACTGCCCTTACC 15

Search completed: June 21, 2003, 22:14:35
 Job time : 284.094 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 76.7812 Seconds
(without alignments)
410.621 Million cell updates/sec

Title: US-09-964-666-12
Perfect score: 14
Sequence: 1 CACTGCACCTTCCA 14

Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:.*
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19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:.*
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21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13	92.9	25	19	AAV23155
C 2	13	92.9	27	20	AAV23155
C 3	11.4	81.4	20	24	AAV23155
C 4	11.4	81.4	22	24	AAV23155
C 5	11.4	81.4	27	9	AAV23155
C 6	11.4	81.4	27	9	AAV23155
C 7	11.4	81.4	31	22	AAV23155
C 8	11.4	81.4	36	14	AAV23155
C 9	11.4	81.4	41	22	AAV23155

C 10	11	78.6	20	21	AAV23155	Dog genomic marker
C 11	11	78.6	20	24	AB194202	Capture oligonucleotide
C 12	11	78.6	20	24	AB196798	Capture oligonucleotide
C 13	11	78.6	24	24	AB184974	Capture oligonucleotide
C 14	11	78.6	24	24	AB184975	Capture oligonucleotide
C 15	11	78.6	24	24	AB190166	Capture oligonucleotide
C 16	11	78.6	24	24	AB190167	Capture oligonucleotide
C 17	11	78.6	28	21	AAV14469	Human PA12 PCR pri
C 18	11	78.6	47	24	ABK40815	Human obesity-asso
C 19	10.6	75.7	31	20	AAV06147	Human biallelic po
C 20	10.4	74.3	13	23	ABH25832	Oligonucleotide SE
C 21	10.4	74.3	13	23	ABH25833	Oligonucleotide SE
C 22	10.4	74.3	17	20	AAV90213	Human yes1 biallel
C 23	10.4	74.3	18	19	AAV62716	Nucleotide sequenc
C 24	10.4	74.3	18	21	AAV73123	Human biallelic ma
C 25	10.4	74.3	18	24	ABH92015	Human stromelysin-
C 26	10.4	74.3	20	16	AAV95921	Primer A (Group 13
C 27	10.4	74.3	20	22	AAV10648	Human caspase 3 an
C 28	10.4	74.3	20	22	AAH80505	Oligonucleotide hy
C 29	10.4	74.3	20	22	AAH80506	Oligonucleotide hy
C 30	10.4	74.3	20	22	AAH80507	Oligonucleotide hy
C 31	10.4	74.3	20	22	AAH80508	Oligonucleotide hy
C 32	10.4	74.3	20	22	AAH80509	Oligonucleotide hy
C 33	10.4	74.3	20	22	AAH80510	Oligonucleotide hy
C 34	10.4	74.3	20	22	AAH80511	Oligonucleotide hy
C 35	10.4	74.3	20	22	AAH80512	Oligonucleotide hy
C 36	10.4	74.3	20	22	AAH63063	Shrimp white spot
C 37	10.4	74.3	20	24	ABK14343	Human interleukin-
C 38	10.4	74.3	21	17	AAV34465	Primer used in alc
C 39	10.4	74.3	21	17	AAV17610	Human arylsulphata
C 40	10.4	74.3	21	21	AAH49891	Zs1966 sequencing
C 41	10.4	74.3	21	22	AAV73538	Human GPR21 DNA P
C 42	10.4	74.3	21	22	AAH25541	PCR primer used to
C 43	10.4	74.3	21	24	ABH35625	Nicotiana benthami
C 44	10.4	74.3	22	20	AAV28746	Primer RT-R6 for d
C 45	10.4	74.3	22	20	AAV45623	PCR primer RT-R6 f

ALIGNMENTS

RESULT 1
AAV23155/c
ID AAV23155 standard; DNA; 25 BP.
XX
AC AAV23155;
XX
DT 23-JUL-1998 (first entry)
XX
DE Primer -1299/-1/CAT for human CD95 gene.
XX
KW CD95; regulatory region; silencer; enhancer; apoptosis; inhibitor;
KW cancer; viral infection; neurodegeneration; autoimmune disease; human;
KW gene therapy; transcription factor; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9808965-A2.
XX
PD 05-MAR-1998.
XX
PF 23-AUG-1997; 97WO-NZ00107.
XX
PR 30-AUG-1996; 96US-0713557.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Rudert F, Watson JD;
XX
DR WPI; 1998-179445/16.
XX
PT New regulatory regions from the CD95 gene and transcription factors

PT that interact with them - for control of apoptosis, e.g. in
PT treatment of cancer, viral infection, neurodegeneration and
PT auto-immune disease
XX
PS Disclosure; Page 40; 60pp; English.
XX
CC This sequence is a primer for the CD95 gene, and is used to isolate the
CC regulatory nucleic acids of the invention. The regulatory regions
CC (silencers or enhancers) are involved in apoptosis, e.g. inhibition of
CC CD95 expression will inhibit apoptosis. Regulation of apoptosis is useful
CC in treatment of cancer, (retroviral infection, neurodegeneration and
CC autoimmune disease, e.g. by gene therapy for expressing transcription
CC factors or expression of antisense sequences to inhibit transcription
CC factor production. The regulatory nucleic acids and transcription factors
CC are also useful for studying regulation of CD95 in vitro or in vivo, to
CC screen for modulators and as probes to isolate related genes.
XX
SO Sequence 25 BP; 6 A; 4 C; 9 G; 6 T; 0 other;
Query Match 92.9%; Score 13; DB 19; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CACTGCACCTTNCCA 14
Db 23 CACTGCACCTTACCA 10
IIIIIIIIIIII
RESULT 2
AAx84455/c
ID AAx84455 standard; DNA: 27 BP.
XX
AC AAx84455;
XX
DT 10-SEP-1999 (first entry)
XX
DE PCR primer for BCNG coding sequence.
XX
XX BCNG; brain cyclic nucleotide gated ion channel; epilepsy; hyperalgesia;
XX Alzheimer's Disease; Parkinson's Disease; long QT syndrome; dyslexia;
XX sick sinus syndrome; age-related memory loss; cystic fibrosis;
XX sudden death syndrome; pacemaker rhythm dysfunction; sensory disorder;
XX auditory disorder; respiratory disorder; attention deficit disorder;
XX learning disability; drug addiction; therapy; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO9932615-A1.
XX
XX 01-JUL-1999.
XX
XX 23-DEC-1998; 98WO-US27630.
XX
XX 28-MAY-1998; 98US-0086436.
XX
XX 23-DEC-1997; 97US-0997685.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX PA
XX PI Bartsch D, Grant S, Kandel ER, Santoro B, Siegelbaum S;
XX PT Tibbs G;
XX DR WPI; 1999-418922/35.
XX
XX An isolated nucleic acid encoding a brain or heart cyclic
XX nucleotide-gated ion channel
XX
XX Claim 24; Page 205; 213pp; English.
XX
XX This sequence is a PCR primer for DNA encoding the brain cyclic
XX nucleotide-gated ion channel (BCNG) of the invention. BCNG and
XX BCNG-related proteins are useful in screening for compounds that
XX modulate, interact or affect expression. Compounds, e.g. antagonists and
XX agonists, identified in the methods are useful for modulating BCNG or

CC BCNG-related protein activity. Modulation is increased or decreased ion
CC permissivity or ion flow rate. Modulators of BCNG can be used to treat a
CC neurological, renal, pulmonary, hepatic or cardiovascular condition. Such
CC conditions include epilepsy, Alzheimer's Disease, Parkinson's Disease,
CC long QT syndrome, sick sinus syndrome, age-related memory loss, cystic
CC fibrosis, sudden death syndrome or pacemaker rhythm dysfunction. BCNG or
CC BCNG-related protein can also be used to treat sensory disorders,
CC e.g. blindness, loss of vision, loss of smell, numbness and lack of
CC ability to taste. Also treatable are auditory disorders, respiratory
CC disorders due to defects in central nervous system areas that control
CC respiration or defects in the lungs, dyslexia, attention deficit disorder
CC or learning disabilities, drug addiction and regulation of cell
CC secretions. The proteins are useful targets for screening for drugs that
XX are effective in the control of pain and hyperalgesia.
XX
SO Sequence 27 BP; 6 A; 7 C; 9 G; 5 T; 0 other;
Query Match 92.9%; Score 13; DB 20; Length 27;
Best Local Similarity 92.9%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CACTGCACCTTNCCA 14
Db 21 CACTGCACCTTGCCA 8
IIIIIIIIIIII
RESULT 3
ABK44429
ID ABK44429 standard; DNA: 20 BP.
XX
AC ABK44429;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human HPR/GCK-like kinase antisense oligonucleotide, ISIS 105328.
XX
XX Human; HPR/GCK-like kinase; antiinflammatory; cytostatic; antimicrobial;
XX HGR; NIK; Nck-interacting kinase; infection; inflammation; tumour;
XX antisense gene therapy; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX modified_base 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone; all cytidines
XX are 5-methylcytidines"
XX
XX modified_base 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "Optionally 2'-methoxyethyl (2'WOE) nucleotides"
XX
XX PN US6346416-B1.
XX
XX 12-FEB-2002.
XX
XX 29-AUG-2000; 2000US-0651011.
XX
XX 29-AUG-2000; 2000US-0651011.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PA
XX PI Dean NM, Cowsett LM;
XX PT WPI; 2002-237091/29.
XX
XX New antisense compound, useful for preventing or delaying infection,

PT inflammation or tumour formation, is targeted to nucleic acid molecule
PT encoding HPK/GCK-like kinase (HGK) and hybridises and inhibits HGK
PT expression
PS Claim 14: Column 43-44; 37pp; English.
XX
CC The invention relates to an antisense compound (I) of 8-50 nucleobases in
CC length targeted to a start codon region, coding region or 3'-untranslated
CC region of a nucleic acid molecule encoding HPK/GCK (undefined)-like
CC kinase (HGK) (also known as NIK for NIK-interacting kinase), which
CC specifically hybridises with and inhibits expression of HGK. (I) is
CC useful for inhibiting the expression of HPK/GCK-like kinase in cells or
CC tissues in vitro. (I) is useful prophylactically e.g. to prevent or delay
CC infection, inflammation and tumour formation. (I) is also useful as a
CC diagnostic and research reagent. (I) is also useful for distinguishing
CC functions of various members of a biological pathway and in
CC antisense gene therapy. The present sequence represents an antisense
CC oligonucleotide targeted to human HPK/GCK-like kinase.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 other;
XX
Query Match 81.4%; Score 11.4; DB 24; Length 20;
Best Local Similarity 85.7%; Pred. No. 3e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CACTGCACCTTNCCA 14
DB 1 CACTGCACCTTNCCA 14
RESULT 4
AAS03611
ID AAS03611 standard; DNA; 22 BP.
XX
AC AAS03611;
XX
DT 29-AUG-2001 (first entry)
XX
DE PCR primer rend9b1, used to detect RHD positive haplotypes.
XX
XX
KM Rhesus box; RHD positive; sequence length polymorphism; SSP; RHD; SMP1;
KM RHCE; RHD negative; blood group typing; blood transfusion; antigen C;
KM haemolytic disease of the newborn; chromosome 1 p34.1-p36; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200132702-A2.
XX
PD 10-MAY-2001.
XX
PF 31-OCT-2000; 2000MO-EP10745.
XX
PR 02-NOV-1999; 99EP-0121686.
PR 31-MAY-2000; 2000EP-0111696.
XX
PA (DRKB-) DRK BLUTSPENDEDIENST BADEN WÜRTTEMBERG.
XX
PI Flegel WA, Wagner FF;
XX
DR WPI: 2001-291052/30.
XX
PT New nucleic acid molecular structure, useful for detection of common
PT RHD positive haplotypes in D-negative individuals, comprises RHD, SMP1
PT and RHCE genes
XX
PS Example 13; Page 56; 135pp; English.
XX
CC The sequence represents PCR primer rend9b1, used to detect RHD positive
CC haplotypes in RHD negative individuals. The primer was used in DNA
CC typing using PCR-sequence length polymorphism (SSP) of the Rhesus genes
CC locus comprising the RHD, SMP1 and RHCE (all undefined) genes and/or the
CC Rhesus box(es), preferably the hybrid Rhesus box, the upstream Rhesus box
CC and/or the downstream Rhesus box. The RHD and RHCE genes are located at

CC chromosome 1 p34.1-p36. Rhesus box flanks the breakpoint region of the
CC RHD deletion in the common RHD negative haplotypes. The primers of the
CC invention are useful for: (1) the specific detection of the common RHD
CC positive haplotypes in D-negative individuals; (2) blood group typing;
CC (3) determining whether a patient can be transfused with Rhd negative
CC blood and whether blood is suitable for transfusion to patients who
CC should not be exposed to antigen C; (4) assessing the risk of a Rhd
CC negative mother of conceiving or carrying an Rhd positive foetus. Anti-D
CC antibodies are useful for treating pregnant women who are Rhesus D
CC negative, where the foetus is not homozygous for the RHD gene to treat
CC or prevent haemolytic disease of the newborn.
XX
SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
XX
Query Match 81.4%; Score 11.4; DB 22; Length 22;
Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 CACTGCACCTTNCCA 14
DB 1 CACTGCACCTTGCGA 14
RESULT 5
AAN81248
ID AAN81248 standard; DNA; 27 BP.
XX
AC AAN81248;
XX
DT 14-SEP-1990 (first entry)
XX
DE Probe 0-YNH24 to identify intrinsic polymorphism of loci in human DNA.
XX
DE Synthetic probe; restriction fragment length polymorphism;
KM paternity testing; ss.
XX
OS Synthetic.
XX
PN EP294098-A.
XX
PD 07-DEC-1988.
XX
PF 26-MAY-1988; 88EP-0304763.
XX
PR 17-MAY-1988; 88US-0194982.
XX
PA (CITY) CITY OF HOPE MED CENTRE.
XX
PI Wallace RB;
XX
DR WPI: 1988-347751/49.
XX
PT New oligonucleotide hybridisation probe specific for repeat units
PT with high specificity for single locus, useful e.g. in paternity testing.
XX
PS Claim 7(e); Page 6; 9pp; English.
XX
CC Total length: 27.
CC Length repeat unit: 31.
CC No. repeat units: 1.
CC Category of hybridisation to human DNA: 1.
CC The probe is complementary to one or two repeat units of VTNR loci.
CC genomic DNA, eg for paternity testing, diagnosing cancer or genetic
CC diseases, and studying post-bone marrow transplant chimerism. Under high
CC criteria, it yields a locus-specific or multi-loci, polymorphic
CC hybridisation pattern, and is more specific for a single locus (or small
CC no. of loci) than known probes.
XX
SQ See also N981243-53.
XX
Query Match 81.4%; Score 11.4; DB 9; Length 27;

Best Local Similarity 85.7%; Pred. No. 3.1e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCCA 14
14 CACTGCACCTTNCCA 27

RESULT 6

AA82045
ID AAN82045 standard; DNA; 27 BP.

AC AAN82045;

DT 12-DEC-1990 (first entry)

DE Probe O-YNH24 for human genomic DNA.

KW Synthetic oligonucleotide; probe O-YNH24; ss DNA; human genomic DNA.

PN EP294098-A.

PD 07-DEC-1998.

PF 26-MAY-1988; 88EP-0304763.

PR 29-MAY-1987; 87US-0055224.

PR 17-MAY-1988; 88US-0194982.

PA (CITY) CITY OF HOPE.

PI Wallace RB;

DR WPI; 1988-34751/49.

PT New Oligonucleotide hybridisation probe specific for repeat units -

PT with high specificity for single locus, useful e.g. in paternity

PS Claim 7; page 6; 8pp; English.

CC The probe is used for genetic identification of a sample of human genomic

CC DNA, e.g. for paternity testing, diagnosing cancer or genetic diseases,

CC and studying bone marrow transplant chimerism. Under high criteria it

CC yielded locus-specific or multi-loci, polymorphic hybridisation pattern,

CC and is more specific for a single locus (or small number of loci) than

CC known probes.

SQ Sequence 27 BP; 7 A; 12 C; 2 G; 6 T; 0 other;

OY 1 CACTGCACCTTNCCA 14
14 CACTGCACCTTNCCA 27

RESULT 7

AA504026
ID AAS04026 standard; DNA; 31 BP.

AC AAS04026;

DT 12-SEP-2001 (first entry)

DE VNTR hybridisation probe, minisatellite YNH24.

KW Human: probe: hypervariable number of tandem repeat: VNTR:

KW species identification; virus detection; minisatellite YNH24;

KW Epstein-Barr virus; ds.

OS Homo sapiens.

FX Key Location/Qualifiers

FT modified_base 31

FT +tag= a /note= "labelled with 4'-6-diamidino-2-phenylindole"

PN US6238866-BI.

PD 29-MAY-2001.

PF 08-FEB-1999; 99US-0246277.

PR 16-APR-1996; 96US-0015965.

PR 16-APR-1997; 97US-0038157.

PA (USSA) US SEC OF ARMY.

PI Yeh HR, Wick CH;

DR WPI; 2001-366471/38.

PT New device with a panel of double stranded oligonucleotide probes

PT immobilized on a solid support, useful for detecting or characterizing

PT a nucleic acid analyte without requiring electrophoresis or the direct

PT sequencing of analyte

PS Example 1; Column 20; 24pp; English.

CC The sequence represents the nucleotide sequence of variable number of

CC tandem repeats (VNTR) hybridisation probe, minisatellite YNH24. The

CC sequence was used as a probe to demonstrate the method of the invention,

CC which is a device for detecting or characterizing a nucleic acid

CC analyte. The device comprises a panel of double stranded oligonucleotide

CC probes immobilised on a solid support. Each probe has a first strand

CC comprising a hypervariable number of tandem repeat sequences and a second

CC strand complementary to the first strand. The probe is selected to

CC hybridise to at least one allele of the nucleic acid analyte and

CC comprises a fragment of an Epstein-Barr virus genome spanning from

CC nucleotide 7421-8042. The device is useful for detecting or

CC characterising a nucleic acid analyte without requiring electrophoresis

CC or the direct sequencing of analyte samples or analyte fragments. The

CC device is particularly useful for individual and species identification.

CC The device is simple and reliable compared to those previously used in

CC prior methods. The device is also readily applied outside of a laboratory

CC environment, such as detection of pathogenic virus strains under

CC emergency conditions in the field.

SQ Sequence 31 BP; 7 A; 14 C; 3 G; 7 T; 0 other;

OY 1 CACTGCACCTTNCCA 14
9 CACTGCACCTTNCCA 22

RESULT 8

AAQ49016
ID AAQ49016 standard; DNA; 36 BP.

AC AAQ49016;

DT 22-APR-1994 (first entry)

DE Multimeric (SBP) antibody chain primer.

KW SBP: specific binding pair members: antibody; RCDP:

KW replicable genetic display package; recombination; PCR:

KW polymerase chain reaction; ss.

OS Synthetic.
 XX
 PN WO9319172-A.
 XX
 PD 30-SEP-1993.
 XX
 PF 24-MAR-1993; 93WO-GB00605.
 XX
 PR 24-MAR-1992; 92GB-0006318.
 PR 15-MAY-1992; 92MO-GB00883.
 XX
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MEDICAL RES. COUNCIL.
 PI Griffiths AD, Johnson KS, Smith AJH, Waterhouse P;
 PI Winter GP;
 DR WPI: 1993-320739/40.
 XX
 PT Prodn. of specific binding pair members, e.g. antibody chains -
 PT by display on surface of replicable genetic display packages
 PS
 PS Disclosure: Page 58; 81pp; English.
 CC The primers (AAQ48987-Q49045) are used in the amplification of Kappa
 CC and lambda-chain genes of various antibodies. These genes are then
 CC recombed into the same replicon, resulting in very diverse libraries
 CC of antibody chains, e.g. from unimmunised donors. It is also useful
 CC for chain shuffling, mutagenesis, humanising and CDR imprinting.
 XX
 SQ Sequence 36 BP; 10 A; 13 C; 7 G; 6 T; 0 other;

Query Match 81.4%; Score 11.4; DB 14; Length 36;
 Best Local Similarity 85.7%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACTTNCCA 14
 |||||
 DB 9 CAGTGCACCTGCCA 22

RESULT 9
 AAH46243
 ID AAH46243 standard; DNA; 41 BP.
 XX
 AC AAH46243;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human neuronal thread protein 17 probe, SEQ ID NO:8.
 XX
 KW Human neuronal thread protein 17; recombinant production;
 KW malignant tumour; cancer; blood disease; HIV infection;
 KW human immunodeficiency virus; immune disorder; inflammatory condition;
 KW cytosolic; anti-HIV; antiinflammatory; immunomodulator; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200146237-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 18-DEC-2000; 2000MO-CN00585.
 PR 22-DEC-1999; 99CN-0125691.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI: 2001-441667/47.
 XX
 PT Human neuronal thread protein 17 and encoded polynucleotide, applicable

PT in diagnosis and treatment of cancer, hemopathy, HIV infection,
 PT immunological diseases and phlogosis
 XX
 XX Example 7; Page 17; 40pp; Chinese.
 PS
 CC The invention relates to human neuronal thread protein 17 (AAB98894),
 CC nucleic acids encoding it (AAH46238), and a method for the recombinant
 CC production of the protein. The present invention additionally discloses
 CC an antagonist of neuronal thread protein 17 for therapeutic use, and an
 CC antibody which specifically binds to neuronal thread protein 17. Neuronal
 CC thread protein 17, and nucleotides which encode it may be used for
 CC treating a variety of diseases, such as malignant tumours, blood
 CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
 CC and inflammatory conditions. The protein may also be used to screen for
 CC modulators of its activity or for peptide fingerprinting identification.
 CC The polynucleotide can be used as a primer for nucleic acid amplification
 CC reactions or as a probe for hybridisation reactions, or in producing gene
 CC chips or microarrays. Sequences AAH46243-AAH46244 represent human
 CC neuronal thread protein 17 probes used in an exemplification of the
 CC invention.
 XX
 SQ Sequence 41 BP; 9 A; 12 C; 10 G; 10 T; 0 other;

Query Match 81.4%; Score 11.4; DB 22; Length 41;
 Best Local Similarity 85.7%; Pred. No. 3.3e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACTTNCCA 14
 |||||
 DB 28 CACTGCATTTCCA 41

RESULT 10
 AA66165
 ID AA66165 standard; DNA; 20 BP.
 XX
 AC AA66165;
 XX
 DT 09-OCT-2000 (first entry)
 XX
 DE Dog genomic marker oligonucleotide sequence SEQ ID NO:27.
 XX
 KW Dog; genome; genomic marker; radiation hybrid map; identification;
 KW chromosome location; gene marker; polymorphic microsatellite marker;
 KW phenotype; behaviour; pedigree; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO200029615-A2.
 XX
 PD 25-MAY-2000.
 XX
 PF 15-NOV-1999; 99WO-IB01907.
 PR 13-NOV-1998; 98US-0108193.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Galibert F, Andre C;
 XX
 DR WPI: 2000-387821/33.
 XX
 PT New radiation hybrid map of the dog, Canine familiaris, genome, useful
 PT for e.g. identifying genes implicated in phenotypic and behavioral
 PT traits or in genetic diseases and for studying dog pedigrees
 PS
 PS Claim 1; Page 54; 87pp; English.
 XX
 CC The present invention describes a radiation hybrid map of the dog
 CC (Canine familiaris) genome comprising the genome location of a marker
 CC selected from AA66139 to AA66942. The radiation hybrid map is useful
 CC for identifying and localising dog genes, since it covers approximately
 CC 80 % of the dog genome and provides a dense map integrating different

CC types (i.e. Type I and Type II) of markers. The map and the dog genome
CC markers (or complementary sequences) are especially useful to identify
CC genes responsible for phenotypic and behavioural traits in dogs, to
CC identify morbid genes, to analyse diseases and identify implicated genes
CC in such diseases and their alleles, and to study dog pedigrees. They
CC may also be useful for isolating corresponding human gene sequences
CC e.g. genes involved in genetic diseases.
XX
SQ Sequence 20 BP; 4 A; 9 C; 2 G; 5 T; 0 other;
Query Match 78.6%; Score 11; DB 21; Length 20;
Best Local Similarity 91.7%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 ACTGCACCTTCC 13
 |||||
DB 9 ACTGCACCTTCC 20
RESULT 11
ABI94202/c
ID ABI94202 standard; DNA: 20 BP.
XX
AC ABI94202;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#1289 oligo #9.
XX
KW Human: K-ras; PCR primer: probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PE 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kilman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food

CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 20;
Best Local Similarity 91.7%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 CTGCACCTTCCA 14
 |||||
DB 18 CTGCACCTTGCCA 7
RESULT 12
ABI96798/c
ID ABI96798 standard; DNA: 20 BP.
XX
AC ABI96798;
XX
DT 16-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#3885 oligo #9.
XX
KW Human: K-ras; PCR primer: probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PE 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kilman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 29; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food

```
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
CC
XX
SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 20;
Best Local Similarity 91.7%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CACTGCACCTTNC 12
Db 16 CACTGCACCTTGC 5

RESULT 13
AB184974/c
ID AB184974 standard; DNA: 24 BP.
XX
AC AB184974;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1289 oligo #1.
XX
KW Human: K-ras: PCR primer; probe; capture probe: mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
```

```
CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB182074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
CC
XX
SQ Sequence 24 BP; 6 A; 8 C; 7 G; 3 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 24;
Best Local Similarity 91.7%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 CTGCACCTTNC 14
Db 22 CTGCACCTTGCCA 11

RESULT 14
AB184975
ID AB184975 standard; DNA: 24 BP.
XX
AC AB184975;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide Zip ID#1289 oligo #2.
XX
KW Human: K-ras: PCR primer; probe; capture probe: mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensic;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR ) CORNELL RES FOUND INC.
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
PI Barany F, Zivvi M, Gerry NP, Favis R, Kliman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (I) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medinensis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food
```

CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB192074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 3 A; 7 C; 8 G; 6 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 24;
Best Local Similarity 91.7%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 CTGCACCTTCCA 14
|||||
Db 3 CTGCACCTTGCCA 14
RESULT 15
AB190166/c
ID AB190166 standard; DNA; 24 BP.
XX
AC AB190166;
XX
DT 15-FEB-2002 (first entry)
XX
DE Capture oligonucleotide zip ID#3885 oligo #1.
XX
KW Human; K-ras; PCR primer; probe; capture probe; mutation detection;
KW ligase detection reaction; LDR; p53; BRCA1; BRCA2; infectious disease;
KW infection; 21 hydroxylase deficiency; Turner Syndrome; obesity;
KW cancer; oncogene; tumour suppressor; human papillomavirus; forensis;
KW environmental monitoring; food industry; feed industry; ss.
XX
OS Synthetic.
XX
PN WO200179548-A2.
XX
PD 25-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10958.
XX
PR 14-APR-2000; 2000US-197271P.
XX
PA (CORR) CORNELI RES FOUND INC.
XX
PI Barany F, Zilva M, Gerry NP, Favis R, Kliman R;
XX
DR WPI: 2002-034366/04.
XX
PT Designing capture oligonucleotide probes for use on a support to which
XX complementary oligonucleotides hybridize with little mismatch -
XX
PS Example 5; Fig 25; 300pp; English.
XX
CC The present invention describes a method (M1) for designing capture
CC oligonucleotide probes (I) for use on a support to which complementary
CC oligonucleotide probes (II) will hybridise with little mismatch, where
CC (i) have melting temperatures within a narrow range. The method is useful
CC for detecting infectious diseases caused by bacterial infectious agents
CC e.g. Salmonella, Listeria monocytogenes and Haemophilus influenza, fungal
CC infectious agents e.g. Cryptococcus neoformans, Candida albicans and
CC Aspergillus fumigatus, viruses e.g. T-cell lymphocytotropic virus,
CC Epstein-Barr virus and polio virus, and parasitic infectious agents
CC selected from Onchocerca volvulus, Entamoeba histolytica and Dracunculus
CC medialis. The method is also useful for detecting genetic diseases such
CC as 21 hydroxylase deficiency, Turner Syndrome and obesity defects.
CC Detecting cancer involving oncogenes, tumour suppressor genes, or genes
CC involved in DNA amplification, replication, recombination or repair, the
CC cancer is specifically associated with a gene selected from BRCA1 gene,
CC p53 gene, human papillomavirus types 16 and 18 and liver cancers. The
CC method is also used for environmental monitoring, forensics and the food

CC and feed industry, detecting comprises scanning (using e.g. a scanning
CC electron microscope and infrared microscope) the support at the
CC particular sites and identifying if ligation of the oligonucleotide probe
CC sets occurred and correlating (using a computer) identified ligation to a
CC presence or absence of the target nucleotide sequences. AB192074 to
CC AB197546 represent oligonucleotide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 24 BP; 4 A; 7 C; 8 G; 5 T; 0 other;
Query Match 78.6%; Score 11; DB 24; Length 24;
Best Local Similarity 91.7%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CACTGCACCTTNC 12
|||||
Db 16 CACTGCACCTTGC 5

Search completed: June 21, 2003, 22:26:25
Job time : 79.7812 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 16.625 Seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-12
Perfect score: 14
Sequence: 1 CACTGCACCTNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata1/1na/6B_COMB.seq:*
5: /cgn2_6/prodata1/1na/PCRTUS_COMB.seq:*
6: /cgn2_6/prodata1/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	13	92.9	25	2	US-08-713-557B-23
2	11.4	81.4	20	4	US-09-651-011A-29
3	11.4	81.4	31	4	US-09-246-277A-7
4	11.4	81.4	36	1	US-08-307-619-37
5	11.4	81.4	36	2	US-08-350-260A-83
6	11.4	81.4	36	2	US-08-350-260A-120
7	11.4	81.4	36	3	US-09-050-783-37
8	10.4	74.3	18	1	US-08-362-706A-2
9	10.4	74.3	18	4	US-09-549-808-2
C 10	10.4	74.3	20	4	US-09-021-701-469
C 11	10.4	74.3	20	4	US-09-021-701-470
C 12	10.4	74.3	20	4	US-09-021-701-471
C 13	10.4	74.3	20	4	US-09-021-701-472
C 14	10.4	74.3	20	4	US-09-021-701-473
C 15	10.4	74.3	20	4	US-09-021-701-474
C 16	10.4	74.3	20	4	US-09-021-701-475
C 17	10.4	74.3	20	4	US-09-021-701-476
C 18	10.4	74.3	20	4	US-09-484-617-148
C 19	10.4	74.3	21	1	US-08-299-187-2
C 20	10.4	74.3	21	4	US-09-495-797-31
C 21	10.4	74.3	21	5	PCR-US95-1111A-2
C 22	10.4	74.3	22	2	US-09-056-691-4
C 23	10.4	74.3	22	3	US-08-812-515-4
C 24	10.4	74.3	22	4	US-09-418-720-23
C 25	10.4	74.3	36	1	US-09-384-327-15
C 26	10.4	74.3	36	1	US-08-458-372-15
C 27	10.4	74.3	36	6	5506118-6

28	10.4	74.3	41	1	US-08-307-619-61	Sequence 61, Appl
29	10.4	74.3	41	2	US-08-350-260A-107	Sequence 107, App
30	10.4	74.3	41	2	US-08-350-260A-208	Sequence 208, App
31	10.4	74.3	41	3	US-09-050-783-61	Sequence 61, Appl
32	10.4	74.3	44	2	US-08-350-260A-583	Sequence 583, App
C 33	10	71.4	20	1	US-08-564-002-1	Sequence 1, Appl
C 34	10	71.4	20	3	US-09-047-347-11	Sequence 11, Appl
C 35	10	71.4	20	4	US-09-517-584A-70	Sequence 70, Appl
C 36	10	71.4	20	4	US-09-180-437-231	Sequence 231, App
C 37	10	71.4	20	4	US-09-487-368A-177	Sequence 177, App
C 38	10	71.4	21	1	US-08-136-741-7	Sequence 7, Appl
C 39	10	71.4	22	4	US-09-460-145-6	Sequence 6, Appl
C 40	10	71.4	23	3	US-08-691-045-37	Sequence 37, Appl
C 41	10	71.4	30	4	US-09-000-094-1	Sequence 1, Appl
C 42	10	71.4	30	4	US-09-000-094-39	Sequence 39, Appl
C 43	10	71.4	33	4	US-08-169-715-47	Sequence 47, Appl
C 44	10	71.4	34	2	US-08-485-778-35	Sequence 35, Appl
C 45	10	71.4	34	3	US-08-520-550A-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-08-713-557B-23/C
Sequence 23, Application US/08713557B
Patent No. 5912168
GENERAL INFORMATION:
APPLICANT: Watson, James D.
ATTORNEY/AGENT INFORMATION:
Rudert, Filiz
TITLE OF INVENTION: CD95 REGULATORY GENE SEQUENCES
TITLE OF INVENTION: AND TRANSCRIPTION FACTORS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,557B
FILING DATE: 30-AUG-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Speckman, Ann W
REGISTRATION NUMBER: 31,881
REFERENCE/DOCKET NUMBER: 11000,1004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
US-08-713-557B-23
Query Match 92.9% Score 13; DB 2; Length 25;
Best Local Similarity 92.9% Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
oy 1 CACTGCACCTNCCA 14

Db 23 CACTGCACCTTACCA 10

RESULT 2

US-09-651-011A-29
Sequence 29, Application US/09651011A
Patent No. 6346416
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF HPK/GCK-LIKE KINASE EXPRESSION
FILE REFERENCE: RTS-0168
CURRENT APPLICATION NUMBER: US/09/651,011A
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 29
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-651-011A-29

Query Match 81.4%; Score 11.4; DB 4; Length 20;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACTGCACCTTACCA 14
Db 1 CACTGCACCTTACCA 14

RESULT 3

US-09-246-277A-7
Sequence 7, Application US/09246277A
Patent No. 6238866
GENERAL INFORMATION:
APPLICANT: Yeh, Homer R.; Wick, Charles H.
TITLE OF INVENTION: NOVEL DETECTOR FOR NUCLEIC ACID
TYPING AND METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of the Chief Counsel
STREET: U.S. Army SBCCOM
CITY: APO (EA)
STATE: Maryland
COUNTRY: United States of America
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/246,277A
FILING DATE: 08-Feb-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. John
REGISTRATION NUMBER: 39908
REFERENCE/DOCKET NUMBER: 436-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (410) 436-1158
TELEFAX: (410) 436-2534
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: YNH24 Minisatellite
SEQUENCE DESCRIPTION: SEQ ID NO: 7;
US-09-246-277A-7

Query Match 81.4%; Score 11.4; DB 4; Length 31;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CACTGCACCTTACCA 14
Db 9 CACTGCACCTTACCA 22

RESULT 4

US-08-307-619-37
Sequence 37, Application US/08307619
Patent No. 5733743
GENERAL INFORMATION:
APPLICANT: Johnson, Kevin S
APPLICANT: Winter, Gregory P
APPLICANT: Griffiths, Andrew D
APPLICANT: Smith, Andrew JH
APPLICANT: Waterhouse, P
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF INVENTION: binding pairs
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,619
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: G01N 33/531, G01N 33/68
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: PCT/GB93/00605
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32238
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-307-619-37

Query Match 81.4%; Score 11.4; DB 1; Length 36;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACTTNCA 14
| | | | | | | | | |
Db 9 CAGTGCACCTTGCCA 22

RESULT 5

US-08-350-260A-83
Sequence 83, Application US/08350260A
Patent No. 5962255

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-350-260A-83

Query Match 81.4%; Score 11.4; DB 2; Length 36;

Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACTTNCA 14
| | | | | | | | | |
Db 9 CAGTGCACCTTGCCA 22

RESULT 6

US-08-350-260A-120
Sequence 120, Application US/08350260A
Patent No. 5962255

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Nissim, Ahuva
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605
FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W

REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300

INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:

LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/549,808
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/174,756
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31796
REFERENCE/DOCKET NUMBER: 13265-1233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-7000
TELEFAX: (650) 324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-549-808-2

Query Match 74.3% Score 10.4; DB 4; Length 18;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNC 13
Db 3 CACTGCCCTTACC 15

RESULT 10
US-09-021-701-469/c
Sequence 469, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-8063
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 469:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-469

Query Match 74.3% Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14
Db 20 ACTGCATTNCCA 8

RESULT 11
US-09-021-701-470/c
Sequence 470, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-8063
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 470:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-470

Query Match 74.3% Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14
Db 19 ACTGCATTNCCA 7

RESULT 12
US-09-021-701-471/c
Sequence 471, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 471:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-471

Query Match 74.3%; Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14
Db 18 ACTGCATTNCCA 6

RESULT 13
US-09-021-701-472/c
Sequence 472, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 472:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-472

Query Match 74.3%; Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCATTNCCA 14
Db 17 ACTGCATTNCCA 5

RESULT 14
US-09-021-701-473/c
Sequence 473, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 473:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-473

Query Match 74.3%; Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACTTNCA 14
||||| ||||
Db 16 ACTGCACTTACCA 4

RESULT 15
US-09-021-701-474/C
Sequence 474, Application US/09021701
Patent No. 6251588
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstarr, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 474:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-474

Query Match 74.3%; Score 10.4; DB 4; Length 20;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACTTNCA 14
||||| ||||
Db 15 ACTGCACTTACCA 3

Search completed: June 22, 2003, 00:01:34
Job time: 18.625 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 41.3438 Seconds

(without alignments)
496.907 Million cell updates/sec

Title: US-09-964-666-12

Perfect score: 14

Sequence: 1 CACTGCACTNCCA 14

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues 832576

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	92.9	14	9	US-09-964-667-12
2	13	92.9	14	10	US-09-964-666-12
3	13	92.9	14	10	US-09-964-412-12
4	11.4	81.4	20	9	US-10-105-004-97
5	11.4	81.4	25	9	US-10-215-112-2203
6	11.4	81.4	25	9	US-10-098-263B-65254
7	10.4	74.3	20	9	US-09-784-674-469
8	10.4	74.3	20	9	US-09-784-674-470
9	10.4	74.3	20	9	US-09-784-674-471
10	10.4	74.3	20	9	US-09-784-674-472
11	10.4	74.3	20	9	US-09-784-674-473
12	10.4	74.3	20	9	US-09-784-674-474
13	10.4	74.3	20	9	US-09-784-674-475
14	10.4	74.3	20	9	US-09-784-674-476
15	10.4	74.3	20	9	US-09-887-145-27
16	10.4	74.3	20	9	US-10-181-107-148
17	10.4	74.3	22	9	US-09-996-956-14
18	10.4	74.3	25	9	US-10-215-112-4856
19	10.4	74.3	25	9	US-10-098-263B-30929

20	10.4	74.3	25	9	US-10-098-263B-48658	Sequence 48658, A
21	10.4	74.3	25	9	US-10-098-263B-53671	Sequence 53671, A
22	10.4	74.3	25	9	US-10-098-263B-94806	Sequence 94806, A
23	10.4	74.3	25	9	US-10-098-263B-121462	Sequence 121462, A
24	10.4	74.3	26	9	US-10-121-857-80	Sequence 80, Appl
25	10.4	74.3	30	9	US-10-113-794A-3	Sequence 3, Appl1
26	10.4	74.3	44	10	US-09-988-899-65	Sequence 65, Appl
27	10.4	74.3	45	9	US-09-905-291A-275	Sequence 275, App
28	10.4	74.3	45	9	US-09-902-853-275	Sequence 275, App
29	10.4	74.3	45	9	US-09-907-824-275	Sequence 275, App
30	10.4	74.3	45	9	US-09-907-841-275	Sequence 275, App
31	10.4	74.3	45	9	US-09-904-011-275	Sequence 275, App
32	10.4	74.3	45	9	US-09-906-742-275	Sequence 275, App
33	10.4	74.3	45	9	US-09-906-838-275	Sequence 275, App
34	10.4	74.3	45	9	US-09-907-613-275	Sequence 275, App
35	10.4	74.3	45	9	US-09-907-942-275	Sequence 275, App
36	10.4	74.3	45	9	US-09-904-820-275	Sequence 275, App
37	10.4	74.3	45	9	US-09-904-859-275	Sequence 275, App
38	10.4	74.3	45	9	US-09-904-820-275	Sequence 275, App
39	10.4	74.3	45	9	US-09-904-859-275	Sequence 275, App
40	10.4	74.3	45	9	US-09-906-646-275	Sequence 275, App
41	10.4	74.3	45	9	US-09-906-700-275	Sequence 275, App
42	10.4	74.3	45	9	US-09-902-903-275	Sequence 275, App
43	10.4	74.3	45	9	US-09-903-749A-275	Sequence 275, App
44	10.4	74.3	45	9	US-09-903-786-275	Sequence 275, App
45	10.4	74.3	45	9	US-09-902-736-275	Sequence 275, App

ALIGNMENTS

RESULT 1
US-09-964-667-12
Sequence 12, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Mands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment of Preventio
Of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-964-667-12

Query Match 92.9%; Score 13; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
DB 1 CACTGCACCTTNCCA 14

RESULT 2

US-09-964-666-12
Sequence 12, Application US/09964666
Patent No. US20020104108A1
GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-964-666-12

Query Match 92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
DB 1 CACTGCACCTTNCCA 14

RESULT 3

US-09-964-412-12
Sequence 12, Application US/09964412
Patent No. US20020129391A1
GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-09-964-412-12

Query Match 92.9%; Score 13; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTTNCCA 14
DB 1 CACTGCACCTTNCCA 14

RESULT 4

US-10-105-004-97/C

Sequence 97, Application US/10105004

Publication No. US20030105002A1

GENERAL INFORMATION:

APPLICANT: Murray, Jeffrey

Semin, Elena

TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC

AND DIAGNOSTIC USES THEREFOR

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/105,004

FILING DATE: 22-Mar-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/754,477

FILING DATE: 22-Nov-1996

ATTORNEY/AGENT INFORMATION:

```
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-022.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-105-004-97

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 20;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTCCA 14
    ||||| |||
Db 20 CACTGCACCTCCA 7

RESULT 5
US-10-215-112-2203
Sequence 2203, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltman
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2203
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2203

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTCCA 14
    ||||| |||
Db 4 CACGGCATTTCGA 17

RESULT 6
US-10-098-263B-65254
Sequence 65254, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 65254
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
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```
US-10-098-263B-65254

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 9; Length 25;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CACTGCACCTTCCA 14
    ||||| |||
Db 8 CACTGCACCTTACCA 21

RESULT 7
US-09-784-674-469/C
Sequence 469, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Delenstarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 20B0
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 469:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 469:
US-09-784-674-469

Query Match
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ACTGCACCTTCCA 14
    ||||| |||
Db 20 ACTGCATTTCGA 8

RESULT 8
```

US-09-784-674-470/c
Sequence 470, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Deleustarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 2080
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-8063
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 470:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 470:
US-09-784-674-470
Query Match 74.3%; Score 10.4; DB 9; Length 20;
Best Local Similarity 84.6%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 ACTGCACCTTACCA 14
||||| 11111
Db 19 ACTGCATTACCA 7

RESULT 9
US-09-784-674-471/c
Sequence 471, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Deleustarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 2080
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-8063
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 471:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 471:
US-09-784-674-471
Query Match 74.3%; Score 10.4; DB 9; Length 20;
Best Local Similarity 84.6%; Pred. No. 1e+04; 2; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 ACTGCACCTTACCA 14
||||| 11111
Db 18 ACTGCATTACCA 6

RESULT 10
US-09-784-674-472/c
Sequence 472, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
Deleustarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 2080
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 472:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 472:
US-09-784-674-472

Query Match
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
DB 17 ACTGCATTACCA 5

RESULT 11
US-09-784-674-473/c
Sequence 473, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
DeJenstarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 20B0
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 473:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 473:
US-09-784-674-473

Query Match
Best Local Similarity 74.3%; Score 10.4; DB 9; Length 20;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
DB 16 ACTGCATTACCA 4

RESULT 12
US-09-784-674-474/c
Sequence 474, Application US/09784674
Publication No. US20030054346A1
GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
Wolber, Paul K.
DeJenstarr, Glenda C.
Webb, Peter G.
Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
Company M/S 20B0
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,674
FILING DATE: 15-Feb-2001
CLASSIFICATION: No. US20030054346A1 available
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/021,701
FILING DATE: 10-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063
INFORMATION FOR SEQ ID NO: 474:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 474:
US-09-784-674-474

Query Match 74.3%; Score 10.4; DB 9; Length 20;
Best Local Similarity 84.6%; Pred. No. 1e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
||||| |||||
DB 15 ACTGCATTACCA 3

RESULT 13

US-09-784-674-475/c
Sequence 475, Application US/09784674
Publication No. US20030054346A1

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

Wolber, Paul K.

DeJenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784, 674

FILING DATE: 15-Feb-2001

CLASSIFICATION: No. US20030054346A1 available

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/021,701

FILING DATE: 10-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 475:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 475:

US-09-784-674-475

Query Match 74.3%; Score 10.4; DB 9; Length 20;

Best Local Similarity 84.6%; Pred. No. 1e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
||||| |||||
DB 14 ACTGCATTACCA 2

RESULT 14

US-09-784-674-476/c
Sequence 476, Application US/09784674
Publication No. US20030054346A1

GENERAL INFORMATION:

APPLICANT: Shannon, Karen W.

Wolber, Paul K.

DeJenstarr, Glenda C.

Webb, Peter G.

Kincaid, Robert H.

TITLE OF INVENTION: Methods for evaluating oligonucleotide
probe sequences

NUMBER OF SEQUENCES: 1165

CORRESPONDENCE ADDRESS:

ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard

STREET: 3000 Hanover Street

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/784, 674

FILING DATE: 15-Feb-2001

CLASSIFICATION: No. US20030054346A1 available

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/021,701

FILING DATE: 10-FEB-1998

ATTORNEY/AGENT INFORMATION:

NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697

REFERENCE/DOCKET NUMBER: 10971464-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-236-2386

TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 476:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 476:

US-09-784-674-476

Query Match 74.3%; Score 10.4; DB 9; Length 20;

Best Local Similarity 84.6%; Pred. No. 1e+04; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
||||| |||||
DB 13 ACTGCATTACCA 1

RESULT 15

US-09-887-145-27

Sequence 27, Application US/09887145

Publication No. US20030082139A1

GENERAL INFORMATION:

APPLICANT: Kim, Seung U

TITLE OF INVENTION: Immortalized human microglia
cell and continuous cell line

NUMBER OF SEQUENCES: 54

CORRESPONDENCE ADDRESS:

ADDRESSEE: David Prashker, Esq.

STREET: P.O. Box 5387

CITY: Magnolia
STATE: Massachusetts
COUNTRY: USA
ZIP: 01930
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
COMPUTER: Dell PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Microsoft word version 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,145
FILING DATE: 22-Jun-2001
CLASSIFICATION: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: UBC-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-887-145-27

Query Match 74.3%; Score 10.4; DB 9; Length 20;
Best Local Similarity 84.6%; Pred. No. 1e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTGCACCTNCCA 14
Db 7 ACTGCACCTGGCCA 19

Search completed: June 22, 2003, 03:18:21
Job time : 43.3438 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.734 Seconds
(without alignments)
374.936 Million cell updates/sec

Title: US-09-964-666-12
Perfect score: 14
Sequence: 1 CACTGCACCTNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estipl:*
7: em_estiro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	50	9	AU105465
C 2	11	78.6	36	13	AU105465 AU105465
C 3	11	78.6	39	17	B1066024 B1066024
C 4	11	78.6	44	10	AZ936711 2M0193103
C 5	10.4	74.3	22	17	AV962509 AV962509
C 6	10.4	74.3	29	17	AZ309394 1M0013P22
					AZ801886 2M0060103

C 7	10.4	74.3	41	17	A2663066
C 8	10.4	74.3	50	9	AU102646
C 9	10	71.4	34	17	AZ470763
C 10	10	71.4	46	17	AL772108
C 11	10	71.4	47	17	AZ462142
C 12	10	71.4	48	13	B1034300
C 13	10	71.4	49	14	C20876
C 14	9.8	70.0	25	17	AZ481615
C 15	9.8	70.0	26	17	HSREA0309
C 16	9.8	70.0	28	9	AA986325
C 17	9.8	70.0	30	17	AZ968733
C 18	9.8	70.0	31	17	AZ779219
C 19	9.8	70.0	32	17	AZ803519
C 20	9.8	70.0	34	17	AA025283
C 21	9.8	70.0	36	17	AZ484892
C 22	9.8	70.0	37	17	AZ481960
C 23	9.8	70.0	38	17	AZ802603
C 24	9.8	70.0	40	9	AA029741
C 25	9.8	70.0	41	17	AZ628318
C 26	9.8	70.0	42	17	AL765117
C 27	9.8	70.0	43	17	AZ345943
C 28	9.8	70.0	46	9	AA001102
C 29	9.8	70.0	46	14	HA5385
C 30	9.8	70.0	47	17	AZ495722
C 31	9.8	70.0	47	17	BH863663
C 32	9.8	70.0	49	17	AZ758301
C 33	9.8	70.0	50	9	AU102480
C 34	9.8	70.0	50	9	AU102875
C 35	9.8	70.0	50	9	AU103683
C 36	9.4	67.1	27	17	AZ378215
C 37	9.4	67.1	29	17	AZ956998
C 38	9.4	67.1	31	17	AZ369584
C 39	9.4	67.1	35	9	AL799355
C 40	9.4	67.1	36	12	BE729346
C 41	9.4	67.1	38	17	AZ507576
C 42	9.4	67.1	41	17	AZ647118
C 43	9.4	67.1	42	17	AZ939796
C 44	9.4	67.1	43	9	AI496922
C 45	9.4	67.1	43	9	AI583956

ALIGNMENTS

RESULT 1
LOCUS AU105465/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU105465 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION HRC09846, mRNA sequence.
VERSION AU105465
KEYWORDS AU105465.1 GI:13554986
SOURCE EST.
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,T., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL MEDLINE
COMMENT 21270072
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,T., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers

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source
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC09846"
/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumurate treated u937 cells"

BASE COUNT      12 a      12 c      14 g      12 t
ORIGIN

Query Match      85.7%; Score 12; DB 9; Length 50;
Best Local Similarity 92.3%; Pred. No. 2.2e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CACTGCACCTTNC 13
        ||||||||| ||
        32 CACTGCACCTTACC 20

RESULT 2
LOCUS      B0666024      36 bp      mRNA      linear      EST 10-DEC-2001
DEFINITION      B0666024 NIBB Mochii normalized xenopus tailbud library Xenopus
laevis cDNA clone XLO84015 5', mRNA sequence.
ACCESSION      B0666024
VERSION      B0666024.1 GI:17479075
KEYWORDS      EST.
SOURCE      African clawed frog.
ORGANISM      Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodidae; Xenopus.
1 (bases 1 to 36)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .36
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XLO84015"
/clone_1lb="NIBB Mochii normalized Xenopus tailbud
library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; CDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC institute)."

BASE COUNT      12 a      6 c      8 g      10 t
ORIGIN

Query Match      78.6%; Score 11; DB 13; Length 36;
Best Local Similarity 91.7%; Pred. No. 6.9e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 ACTGCACCTTNC 13
        ||||||||| ||
        13 ACTGCACCTTACC 24

RESULT 3
LOCUS      A2936711      39 bp      DNA      linear      GSS 26-APR-2001

```

DEFINITION	2M0193103R Mouse 10kb plasmid UNGC2M library Mus musculus genomic			
ACCESSION	A2936711.1 GI:13795292			
VERSION	GSS.			
KEYWORDS	house mouse;			
SOURCE	Mus musculus.			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
REFERENCE	1 (bases 1 to 39)			
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0193 row: 1 column: 03 Seq primer: CACACAGCAACACACTATGACC Class: plasmid ends High quality sequence stop: 39. Location/Qualifiers 1..39 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UNGCM0193103" /clone_lib="Mouse 10kb plasmid UNGC2M library" /sex="Female" /lab_host="E. coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[gb AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."			
BASE COUNT	10 a	10 c	8 g	11 t
ORIGIN				
Query Match	78.6%	Score 11:	DB 17:	Length 39;
Best Local Similarity	91.7%	Pred. No. 7e+04;		
Matches 11: Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Oy	2	ACGTGCACTTNC	13	
Db	15	ACTGCACTTCC	26	
RESULT 4				
AV965209				
LOCUS	AN965209	44 bp	mrna	linear EST 14-MAR-2002

DEFINITION	AV962509 Nori Satoh unpublished cDNA library, larva Clona intestinalis cDNA clone cllv13117 5', mRNA sequence.			
ACCESSION	AV962509			
VERSION	AV962509.1 GI:19450808			
KEYWORDS	EST.			
SOURCE	Clona intestinalis.			
ORGANISM	Clona intestinalis.			
REFERENCE	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Clona.			
AUTHORS	1 (bases 1 to 44)			
TITLE	Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.			
JOURNAL	Expressed genes in Clona intestinalis			
COMMENT	Unpublished (2000)			
FEATURES	Contact: Nori Satoh			
source	Department of Zoology			
	Kyoto University			
	Sakyo-ku, Kyoto, Kyoto 606-8502, Japan			
	Tel: 81-75-753-4081			
	Fax: 81-75-705-1113			
	Email: satoh@ascidian.zool.kyoto-u.ac.jp.			
	Location/Qualifiers			
	1..44			
	/organism="Clona intestinalis"			
	/db_xref="taxon:7719"			
	/clone="c1v13117"			
	/clone_lib="Nori Satoh unpublished cDNA library, larva"			
	/tissue_type="whole animal"			
	/dev_stage="larva"			
	/note="Vector: pbluescript SK"			
BASE COUNT	9 a	9 c	11 g	15 t
ORIGIN				
Query Match	78.6%	Score 11;	DB 10;	Length 44;
Best Local Similarity	91.7%;	Pred. No. 7.2e+04;		
Matches	11; Conservative	0; Mismatches	1; Indels	0; Gaps
QY	2	ACTGCACTTNGC	13	
	1		11	
Db	2	ACTGCACTTGCC	13	
RESULT 5				
AZ309394/c				
LOCUS	AZ309394	22 bp	DNA	linear
DEFINITION	IM0013P22R Mouse 10kb plasmid U0GC1M library Mus musculus genomic clone U0GC1M0013P22 R, DNA sequence.			
ACCESSION	AZ309394			
VERSION	AZ309394.1	GI:10350335		
KEYWORDS	GSS.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 22)			
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Lougacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss			
	University of Utah Genome Center			
	University of Utah			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000 Std Error: 0.00			
	Plate: 0013 row: P column: 22			
	Seq primer: CACACAGCAAAACAGCTATGACC			
	Class: plasmid ends			

FEATURES	High quality sequence stop: 22.
SOURCE	Location/Qualifiers
	1. 22
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	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="U08100013p2"
	/clone_lib="Mouse 10kb plasmid U08100013p2"
	/sex="Male"
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
	/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9147321149b/AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	5 a 3 c 8 g 6 t
ORIGIN	
Query Match	74.3%, Score 10.4; DB 17; Length 22:
Best Local Similarity	84.6%, Pred. No. 1.3e+05;
Matches	11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
0y	1 CACGCACTTNC 13
	11 1111111 11
Db	14 CAATGCACTTCCC 2
RESULT 6	
LOCUS	AZ801886 29 bp DNA linear GSS 16-FEB-2001
DEFINITION	2M0060I03R Mouse 10kb plasmid U08100013 library Mus musculus genomic
ACCESSION	clone U08100013 R, DNA sequence.
VERSION	AZ801886
KEYWORDS	AZ801886.1 GI:12954209
SOURCE	GSS.
ORGANISM	mus mouse.
REFERENCE	Mus musculus
AUTHORS	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murine; Mus. 1 (bases 1 to 29)
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longaker,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0060 row: 1 column: 03 Seq primer: CACGACGCAACACTTATGACC Class: plasmid ends


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/clone="CAS05488"
/clone_lib="Sugano Homo sapiens cDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"
BASE COUNT
19 a 7 c 16 g 8 t
ORIGIN

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Query Match	74.3%	Score 10.4	DB 9	Length 50
Best Local Similarity	84.6%	Pred. 1.5e+05		
Matches	11: Conservative	0: Mismatches	2: Indels	0: Gaps
OY	1 CACTGCACCTTNC	13		
Db	34 CACTGCCCTTAC	22		

RESULT 9	LOCUS	DEFINITION
A2470763/c	A2470763	34 bp. DNA. Linear. GSS 04-OCT-2000
	1M0285F10	Mouse 10kb plasmid U06C1M library Mus musculus genomic
	clone U06C1M0285F10 F,	DNA sequence.

SOURCE ORGANISM	house mouse Mus musculus
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100	100

REFERENCE
AUTHORS

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts unpublished (2000)
COMMENT	Contact: Robert B. Weiss

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0285 row: F column: 10
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 34.

FEATURES	Location/Qualifiers
source	1. .34

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCGCM0285F10"
/clone_lib="Mouse 10kb plasmid uucgcm library"
sex="Male"

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1/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
2/1ab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
3/note="Vector: pMD44(nlv); Purified genomic DNA from M.
4/musculus C57BL/6J (male) was obtained from the Jackson
5/laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	71.4%	Score 10	DB 17	Length 34
Best local similarity	90.9%	Pred	No 2.2e+05	
Matches	10	Conservative	0	Mismatches 1
				Indels 0
				Gaps 0
QY	4	TGCACTTCCCA	14	
db	13	TGCACTTCCCA	3	

RESULT	LOCUS	DEFINITION
10	AL772108	46 bp DNA linear
AL772108/c	Arbidlopsis thallana T-DNA flanking sequence GK-186B11-014622,	GSS 19-JUN-2002
		genomic survey sequence.

NEW WORDS	655.
SOURCE	thale cress
ORGANISM	<i>Arabidopsis</i>

REFERENCE

Journal of Molecular Evolution 2004, 59:100-104
DOI 10.1007/s00838-004-0001-1
© Springer 2004
Published online: 12 November 2004

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
A new Arabidopsis thaliana T-DNA mutagenised population (GMBI-Kat) for flanking sequence tag based reverse genetics	Unpublished	3 (bases 1 to 46)	Li, Y., Strizhkov, N., Rosso, M. and Weisshaar, B.	Direct Submission	Submitted (17-JUN-2002)	Weisshaar, B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g48150. The sequences are generated at the MPI for Plant Breeding Research in						

the context of the GABI-Kat project. GABI-Kat is a plant genomics program designated 'GABI'.

```

availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-kat/.
location/Qualifiers
1..46
source
/organism="Arabidopsis thaliana"
/strain="Colombia 0"
```

/strain="Colombia 0"
 /db_xref="taxon:3702"
 /clone="GK-186B11-014622"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the *A. thaliana* nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT	15 a	6 c	8 g	17 t
ORIGIN				
Query Match	71.4%; Score 10; DB 17; Length 46			

Best Local Similarity 90.9%; Pred. No. 2.4e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TGCACCTNCCA 14
1111111111
DB 21 TGCACCTTACCA 11

RESULT 11

AZ462142 47 bp DNA linear GSS 04-OCT-2000
LOCUS AZ462142/c
DEFINITION IM0269K14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0269K14 F, DNA sequence.

ACCESSION AZ462142
VERSION AZ462142.1 GI:10620267
KEYWORDS GSS.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 47)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Maimoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0269 row: K column: 14
Seq primer: CGTGTGAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 47.

FEATURES

source

1. .47

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0269K14"

/clone_1lb="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PMDA2nv. Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g147321419b/AF2972.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

12 a 1 c 25 g 9 t

ORIGIN

Query Match

71.4% Score 10; DB 17; Length 47;

Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CACTGCACCTT 10
1111111111
DB 34 CACTGCACCTT 25

RESULT 12

B034300 48 bp mRNA linear EST 06-DEC-2001
LOCUS B034300
DEFINITION B034300 NIBB Mochli normalized Xenopus neurula library Xenopus laevis cDNA clone XL028b09 5', mRNA sequence.

ACCESSION B034300
VERSION B034300.1 GI:17391841
KEYWORDS EST.

SOURCE African clawed frog.
ORGANISM Xenopus laevis

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus. 1 (bases 1 to 48)
AUTHORS Kileyama,A., Terasaka,C., Mochli,M., Ueno,N., Shln-I,T. and Kohara,Y.

TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadasu Shin-I
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

source

1. .48

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="XL028b09"

/clone_1lb="NIBB Mochli normalized Xenopus neurula library"

/tissue-type="whole embryo"

/dev_stage="stage 15"

/note="Vector: pBSRN3; Site_1: NotI; site_2: EcoRI; CDNAs were oligo-primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute)."

BASE COUNT 12 a 13 c 11 g 10 t 2 others

ORIGIN

Query Match 71.4% Score 10; DB 13; Length 48;

Best Local Similarity 90.9%; Pred. No. 2.4e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CTCGACCTTACC 13
1111111111
DB 16 CTCGACCTTACC 26

RESULT 13

C20876 49 bp mRNA linear EST 23-OCT-1996
LOCUS C20876
DEFINITION HUMG50004943 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA sequence.

ACCESSION C20876
VERSION C20876.1 GI:1621986
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 49)
AUTHORS Okubo,K.

TITLE	BodyMap; human gene expression database
JOURNAL	Unpublished (1995)
COMMENT	Contact: Okubo, K.

BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-Oka, Suita, Osaka Pref. 565, Japan
Tel.: 06-877-3111 (ex. 3315)

Human Gene Signature, 3'-directed cDNA sequence. We are not submitting the same cDNA sequence redundantly to DBU since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see <http://www.imcb.osaka-u.ac.jp/bodymap/>. The sequences of the clones represented by this GS sequences is also found there.

FEATURES	Location/Qualifiers
source	1. .49

`/organism="Homo sapiens"`
`/db_xref="taxon:9606"`
`/clone_lib="Human adult (K-Okubo)"`
`/dev_stage="adult"`
`/note="Organ: blood; Vector: 1-gt-11; Site: 1: Eco-R1;`
Monocytes were prepared from blood by ficoll-hypaque,
percoll and T cell rosetting purification steps (purify:
96 %). mRNA was prepared from activated monocytes from a
patient with rheumatoid arthritis. mRNA was reverse
transcribed with M-MLV. Using Eco-R1 linkers cDNA was
cloned into 1-gt-11 vector arms. The cDNA library was
screened by differential hybridization using radioactively
marked ss-cDNA from activated and non-activated
monocytes.

```

Query Match      71.4%: Score 10: DB 14: Length 49;
Best Local Similarity 83.3%: Pred. No. 2.4e+05;
Matches 10: Conservative 0: Mismatches 2: Indels 0: Gaps 0:
OY      1 CACTGCACCTGNC 12
         |||||
Db       9 CACTGCACCTGNC 20

```

RESULT 14					
AZ481615					
LOCUS	AZ481615	25 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	IM0306A03F Mouse 10kb plasmid U08C1M library Mus musculus genomic clone U08C1M0306A03 F, DNA sequence.				

ACCESSION	AZ481615
VERSION	AZ481615.1
KEYWORDS	GSS.
	GI:10642680

SOURCE ORGANISM

REFERENCE
AUTHORS
1, (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	Plasmid inserts
COMMENT	Unpublished (2000) Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std error: 0.00
Plate: 0306 Row: A Column: 03
seq primer: CGTGTGTAACGACGGCCCACT

```

Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25
FEATURES
source

```

```

Class: plasmid ends
High quality sequence stop: 25.
Location/Qualifiers
1. .25
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0306A03"
/clone_1kb="Mouse 10kb plasmid U08C1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notice="Vector: PWD42ny: Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g11473211419b1A129072.1)', a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

BASE COUNT	8 a	6 c	6 g	5 t
ORIGIN				

Query Match	70.0%	Score 9.8	Dr 17	Length 25
Best Local Similarity	78.6%	Pred. No. 2.7e+05		
Matches	11	Conservative	0	Mismatches 3
				Indels 0
				Gaps 0
QY	1 CACTGCACCTTNC	CA 14		
	1			
	5 CGCTGCACCTTCAC	CA 18		
db				

RESULT	15
LOCUS	HSTEA0309
DEFINITION	H.sapiens trapped exon SNA0309, genomic survey sequence.

```

VERSION X85346.1 GI:1008100
KEYWORDS GSS; chromosome 21.

```

SOURCE ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE	AUTHORS
1 (bases 1 to 26)	
Lucenti, D.	Chen, H.M., Shea, D., Samec, S.N., Rutter, M., Christ, R.

TITLE
JOURNAL
000000000

ROSSIET, V., BUCKLER, A., ANTONAKAKIS, S. E. and MCCORMICK, M. K.
Localization of 102 exons to a 2.5 Mb region involved in Down
syndrome
Hum. Mol. Genet. 4 (8), 1305-1311 (1995)

MEDLINE	96090248
PUBMED	7581367
REFERENCE	2 (bases 1 to 26)

AUTHORS	Antonarakis, S. E.	
TITLE	Direct Submission	
JOURNAL	Submitted (14-MAR-1995)	S. E. Antonarakis
		Div of Medical Computing

Univ. and Cantonal Hospital
CH-1211 Geneva, SWITZERLAND

```
FEATURES
source
location/Qualifiers
1..26
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q22.2-22.3"
```

BASE COUNT 2 a /note="trapped exon sequence"
ORIGIN 11 c 4 g 9 t

Query Match 70.0%; Score 9.8; DB 17; Length 26;
Best Local Similarity 78.6%; Pred. No. 2.7e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CACTGCACCTTNCOA 14
1 |||||
DB 12 CCCTGCACCTGTCCA 25

Search completed: June 21, 2003, 23:59:01
Job time : 610.901 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds

(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-13

Perfect score: 14

Sequence: 1 CCAGGTGTAGNCCA 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 841850

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rtd:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_hcgo_hum:*

40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	81.4	50	6 AX190063	AX190063 Sequence
2	11.4	81.4	50	6 AX190065	AX190065 Sequence
3	11	78.6	15	6 AR179980	AR179980 Sequence
4	11	78.6	31	6 AX249591	AX249591 Sequence
5	10.4	74.3	15	6 AR132395	AR132395 Sequence
6	10.4	74.3	15	6 AR132396	AR132396 Sequence
7	10.4	74.3	18	12 AB067924	AB067924 Synthetic
8	10.4	74.3	19	6 AX027079	AX027079 Sequence
9	10.4	74.3	20	4 BOVDIK06	D44507 Bovine DNA,
10	10.4	74.3	20	6 AR099541	AR099541 Sequence
11	10.4	74.3	20	6 AR146442	AR146442 Sequence
12	10.4	74.3	20	6 AR178822	AR178822 Sequence
13	10.4	74.3	20	6 AX298604	AX298604 Sequence
14	10.4	74.3	20	12 AB068080	AB068080 Synthetic
15	10.4	74.3	22	6 AX180631	AX180631 Sequence
16	10.4	74.3	24	6 A47937	A47937 Sequence
17	10.4	74.3	24	6 AR090957	AR090957 Sequence
18	10.4	74.3	24	6 AR176982	AR176982 Sequence
19	10.4	74.3	24	6 AR179992	AR179992 Sequence
20	10.4	74.3	24	6 AX190945	AX190945 Sequence
21	10.4	74.3	25	6 AX029401	AX029401 Sequence
22	10.4	74.3	25	6 AX029413	AX029413 Sequence
23	10.4	74.3	31	6 AR024414	AR024414 Sequence
24	10.4	74.3	31	6 AR091787	AR091787 Sequence
25	10.4	74.3	31	6 AX248592	AX248592 Sequence
26	10.4	74.3	31	6 I71206	I71206 Sequence
27	10.4	74.3	31	6 I83765	I83765 Sequence
28	10.4	74.3	32	6 A57190	A57190 Sequence
29	10.4	74.3	45	6 AR083218	AR083218 Sequence
30	10.4	74.3	45	6 AR083219	AR083219 Sequence
31	10.4	74.3	45	6 AR198841	AR198841 Sequence
32	10.4	74.3	47	6 AX194743	AX194743 Sequence
33	10	71.4	20	6 AX329418	AX329418 Sequence
34	10	71.4	20	6 AX443214	AX443214 Sequence
35	10	71.4	20	6 AX452324	AX452324 Sequence
36	10	71.4	21	6 AR210393	AR210393 Sequence
37	10	71.4	23	6 A30274	A30274 Nisin 2' PCR
38	10	71.4	23	6 I33945	I33945 Sequence
39	10	71.4	24	6 AR090423	AR090423 Sequence
40	10	71.4	24	6 AR197458	AR197458 Sequence
41	10	71.4	24	6 AX447309	AX447309 Sequence
42	10	71.4	25	6 AX042600	AX042600 Sequence
43	10	71.4	25	6 AX201537	AX201537 Sequence
44	10	71.4	26	6 AX037879	AX037879 Sequence
45	10	71.4	26	6 AX110848	AX110848 Sequence

ALIGNMENTS

RESULT 1

AX190063

LOCUS

Sequence 242 from Patent WO0147942.

AX190063

ACCESSION

AX190063.1 GI:15143435

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 50)

REFERENCE

Shinkets,R.A. and Leach,M.

Nucleic acids containing single nucleotide polymorphisms and

methods of use thereof

JOURNAL	Patent: WO 0147942-A 242 05-JUL-2001;									
FEATURES	Curagen Corporation (US)									
SOURCE	Location/Qualifiers									
	1. .50									
	/organism="Homo sapiens"									
	/db_xref="taxon:9606"									
	/note="2 of 2 allelic variants (241 is other entry)"									
misc-feature	25. .26									
	/note="Nucleotide deleted between bases 25 and 26									
	Accession number cg43982025"									
BASE COUNT	9 a 13 c 21 g 7 t									
ORIGIN										
Query Match	81.4%; Score 11.4; DB 6; Length 50;									
Best Local Similarity	85.7%; Pred. No. 6.6e+04;									
Matches 12: Conservative	0; Mismatches 2; Indels 0; Gaps 0;									
QY	1 CCAGGTGTAGNCCA 14									
Db	19 CCAGGTGCAGGCCA 32									
RESULT 2										
AXI90065	50 bp DNA Linear PAT 08-AUG-2001									
LOCUS										
DEFINITION	Sequence 244 from Patent WO0147942.									
ACCESSION	AXI90065									
VERSION	AXI90065.1 GI:15143437									
KEYWORDS										
SOURCE	human.									
ORGANISM	Homo sapiens									
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.									
REFERENCE										
AUTHORS	1 (bases 1 to 50)									
TITLE	Shinkets, R.A. and Leach, M.									
JOURNAL	Nucleic acids containing single nucleotide polymorphisms and									
	methods of use thereof									
	Patent: WO 0147942-A 244 05-JUL-2001;									
FEATURES										
source	Curagen Corporation (US)									
	Location/Qualifiers									
	1. .50									
	/organism="Homo sapiens"									
	/db_xref="taxon:9606"									
	/note="2 of 2 allelic variants (243 is other entry)"									
misc-feature	25. .26									
	/note="Nucleotide deleted between bases 25 and 26									
	Accession number cg43982025"									
BASE COUNT	9 a 13 c 21 g 7 t									
ORIGIN										
Query Match	81.4%; Score 11.4; DB 6; Length 50;									
Best Local Similarity	85.7%; Pred. No. 6.6e+04;									
Matches 12: Conservative	0; Mismatches 2; Indels 0; Gaps 0;									
QY	1 CCAGGTGTAGNCCA 14									
Db	18 CCAGGTGCAGGCCA 31									
RESULT 3										
AXI79980/c	15 bp DNA Linear PAT 20-APR-2002									
LOCUS										
DEFINITION	Sequence 48 from patent US 6333152.									
ACCESSION	ARI79980									
VERSION	ARI79980.1 GI:20222013									
KEYWORDS										
SOURCE	Unknown.									
ORGANISM	Unknown.									
	Unclassified.									
REFERENCE										
AUTHORS	1 (bases 1 to 15)									
TITLE	Vogelstein, B., Kinzler, K.W., Zhang, L. and Zhou, W.									
JOURNAL	Gene expression profiles in normal and cancer cells									
	Patent: US 6333152-A 48 25-DEC-2001;									

FEATURES	Location/Qualifiers
SOURCE	1..15
	/organism="unknown"
BASE COUNT	3 a 5 c 3 g 4 t
ORIGIN	
Query Match	78.6%; Score 11; DB 6; Length 15;
Best Local Similarity	91.7%; Pred. No. 1.3e+05;
Matches	11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	3 AGGTGTAGNCCA 14
	11
Db	14 AGGTGTAGCCCA 3
RESULT 4	
LOCUS	AX249591/c 31 bp DNA linear PAT 28-SEP-2001
DEFINITION	Sequence 1670 from Patent WO0166800.
ACCESSION	AX249591
VERSION	AX249591.1 GI:15864214
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	Cargill,M., Ireland,J.S. and Lander,E.S.
JOURNAL	Human single nucleotide polymorphisms
	Patent: WO 0166800-A 1670 13-SEP-2001;
FEATURES	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
	Location/Qualifiers
	1..31
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
BASE COUNT	7 a 8 c 9 g 6 t 1 others
ORIGIN	
Query Match	78.6%; Score 11; DB 6; Length 31;
Best Local Similarity	91.7%; Pred. No. 1.2e+05;
Matches	11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY	2 CAGCTGTAGNCC 13
	11
Db	14 CAGCTGTAGACC 3
RESULT 5	
LOCUS	ARI32395 15 bp DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 820 from patent US 6194150.
ACCESSION	ARI32395
VERSION	ARI32395.1 GI:14121300
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 15)
TITLE	Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
JOURNAL	Nucleic acid based inhibition of CD40
FEATURES	Patent: US 6194150-A 820 27-FEB-2001;
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DEFINITION Sequence 821 from patent US 6194150.
ACCESSION ARI32396
VERSION ARI32396.1 GI:14121301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 821 27-FEB-2001;
FEATURES
source 1.15
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BASE COUNT 3 a 4 c 5 g 3 t
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Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNC 13
14 CCAGGTGAAGTCC 2

Db 14 CCAGGTGAAGTCC 2

RESULT 7
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LOCUS AB067924 18 bp DNA linear SYN 08-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS-sts627405
at 1p36.
ACCESSION AB067924
VERSION AB067924.1 GI:15128728
KEYWORDS
SOURCE synthetic construct DNA.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Matanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Mochizuki,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source 1.18
Location/Qualifiers
/organism="synthetic construct"
/db xref="taxon:32630"
misc_feature 1.18
/note="forward primer for human STS-sts627405 at 1p36
sts-sts627405 obtained from clones B313L13, B244M15, Human
BAC library RPCI-11"
BASE COUNT 3 a 5 c 7 g 3 t
ORIGIN

Query Match 74.3%; Score 10.4; DB 12; Length 18;
Best Local Similarity 84.6%; Pred. No. 2.9e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNC 13
14 CCAGGTGAAGTCC 2

Db 14 CCAGGTGAAGTCC 2

RESULT 8
AX027079/c
LOCUS AX027079 19 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 37 from Patent WO0040719.
ACCESSION AX027079
VERSION AX027079.1 GI:1018094
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 19)
AUTHORS Bonthron,D. and Markham,A.F.
TITLE Wound healing and orofacial clefting
JOURNAL Patent: WO 0040719-A 37 13-JUL-2000;
BONTHRON DAVID (GB) ; UNIV LEEDS (GB) ; MARKHAM ALEXANDER FRED (GB)
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Location/Qualifiers
/organism="Homo sapiens"
/db xref="taxon:9606"
/note="Oligonucleotide primer"
BASE COUNT 4 a 7 c 5 g 3 t
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Best Local Similarity 84.6%; Pred. No. 2.8e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNC 13
13 CCAGGTGAAGTCC 1

Db 13 CCAGGTGAAGTCC 1

RESULT 9
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LOCUS BOVDIK06 20 bp DNA linear MM 09-FEB-1999
DEFINITION Bovine DNA, microsatellite DIK015 PCR antisense primer.
ACCESSION D44507
VERSION D44507.1 GI:624797
KEYWORDS microsatellite.
SOURCE Bos taurus
ORGANISM Bos taurus
REFERENCE 1 (sites)
AUTHORS Hirano,T., Nakane,S., Matanabe,T., Takeda,H.,
Yamakuchi,H., Morita,M., Barendse,W. and Sugimoto,Y.
TITLE Five bovine polymorphic dinucleotide microsatellite loci (DIK008,
DIK010, DIK015, DIK016 and DIK020)
JOURNAL Anim. Genet. 26 (6), 447-448 (1995)
MEDLINE 96151440
REFERENCE 2 (sites)
AUTHORS Hirano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,
Inoue-Murayama,M., Matanabe,T., Barendse,W. and Sugimoto,Y.
TITLE Characterization of 42 highly polymorphic bovine microsatellite
markers
JOURNAL Anim. Genet. 27 (5), 365-368 (1996)
MEDLINE 97083737
REFERENCE 3 (bases 1 to 20)
AUTHORS Inoue,M., Matanabe,T., Hirano,T., Yamakuchi,H.,
Matanabe,E., Morita,M. and Sugimoto,Y.
TITLE Isolation of microsatellites from Japanese black cattle (Wagyu) and
their application to individual identification and paternity
exclusion
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 20)

AUTHORS Sugimoto, Y.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-1994) Yoshikazu Sugimoto, Japan Live Stock Technology Association, Shiraoka Institute of Animal Genetics; Nishigo Odakura, Nishishirakawa, Fukushima 961, Japan (E-mail: LD103222@niftyserve.or.jp, Tel:0248-25-5641, Fax:0248-25-5725)

FEATURES
 source 1..20
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 ORIGIN

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 Best Local Similarity 84.6%; Pred. No. 2.8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGGTGTAGNCCA 14
 Db 7 CAGGTGTGTCCA 19

RESULT 10
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 DEFINITION Sequence 68 from patent US 6077833.
 ACCESSION AR099541
 VERSION AR099541.1 GI:12809307
 KEYWORDS
 ORGANISM Unknown.
 SOURCE Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett, C., Frank, and Vickers, T. A.
 TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
 JOURNAL Patent: US 6077833-A 68 20-JUN-2000;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 4 a 7 c 5 g 4 t
 ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 20;
 Best Local Similarity 84.6%; Pred. No. 2.8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 Db 2 CCAGGTGAGTCC 14

RESULT 11
 LOCUS ARI146442 20 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 61 from patent US 6218510.
 ACCESSION ARI146442
 VERSION ARI146442.1 GI:15109631
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Sharpe, A.H., Portiello, F., Freeman, G.J. and Nadler, L.M.
 TITLE B7-1 and B7-2 polypeptides
 JOURNAL Patent: US 6218510-A 61 17-APR-2001;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 5 a 6 c 5 g 4 t

ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 20;
 Best Local Similarity 84.6%; Pred. No. 2.8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 Db 1 CCAGGTGAGTCC 13

RESULT 12
 LOCUS ARI178822 20 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 68 from patent US 6319906.
 ACCESSION ARI178822
 VERSION ARI178822.1 GI:20219960
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett, C., Frank, and Vickers, T. A.
 TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
 JOURNAL Patent: US 6319906-A 68 20-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 4 a 7 c 5 g 4 t
 ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 20;
 Best Local Similarity 84.6%; Pred. No. 2.8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 Db 2 CCAGGTGAGTCC 14

RESULT 13
 LOCUS AX298604 20 bp DNA linear PAT 26-NOV-2001
 DEFINITION Sequence 238 from Patent WO0183749.
 ACCESSION AX298604
 VERSION AX298604.1 GI:17128594
 KEYWORDS
 SOURCE Mus sp.
 ORGANISM Mus sp.

REFERENCE 1
 AUTHORS Bachmanov, A.A., Beauchamp, G.K., Chatterjee, A., de Jong, P.J., Li, S., Li, X., Ohmen, J.D., Reed, D.R., Ross, D. and Tordoff, M.G.
 TITLE Gene and sequence variation associated with sensing carbohydrate compounds and other sweeteners
 JOURNAL Patent: WO 0183749-A 238 08-NOV-2001;
 FEATURES Location/Qualifiers
 source 1..20
 BASE COUNT 6 a 5 c 6 g 3 t
 ORIGIN

Query Match 74.3%; Score 10.4; DB 6; Length 20;
 Best Local Similarity 84.6%; Pred. No. 2.8e+05;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGGTGTAGNCCA 14


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Db          4 CAGGTGTAGACCA 16

RESULT 14
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LOCUS      AB068080      20 bp      DNA      linear      SYN 06-AUG-2001
DEFINITION Synthetic construct DNA, forward primer for human STS sts-R272C15F
at 1p36.
ACCESSION  AB068080
VERSION    AB068080.1  GI:15128884
KEYWORDS
SOURCE     synthetic construct DNA.
ORGANISM   synthetic construct
            artificial sequences.
REFERENCE  1
AUTHORS    Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
            and Soeda, E.
            A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
            Genomics 74 (1), 55-70 (2001)
JOURNAL    MEDLINE
REFERENCE  2 (bases 1 to 20)
AUTHORS    Horii, A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
            Location/Qualifiers
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            /db_xref="taxon:32630"
            misc-feature
            1..20
            /note="forward primer for human STS sts-R272C15F at 1p36
            sts-R272C15F obtained from clones B359F10, B272C15,
            B91D18, Human BAC library RPCI-11"
BASE COUNT 1 4 a 4 c 6 g 6 t
ORIGIN
Query Match          74.3%; Score 10.4; DB 12; Length 20;
Best Local Similarity 84.6%; Pred. No. 2.8e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCAGGTGTAGNCC 13
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Db      14 CCAGGTATAGCCC 2

RESULT 15
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LOCUS      AX180631      22 bp      DNA      linear      PAT 06-AUG-2001
DEFINITION Sequence 209 from Patent WO0146391.
ACCESSION  AX180631
VERSION    AX180631.1  GI:15132517
KEYWORDS
SOURCE     synthetic construct.
ORGANISM   synthetic construct.
            artificial sequences.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Osbourne, A. E., Haralampidis, K. and Bryan, G. T.
TITLE      Plant gene
JOURNAL    Patent: WO 0146391-A 209 28-JUN-2001;
            Plant Bioscience Limited (GB)
            Location/Qualifiers
FEATURES   source
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            /db_xref="taxon:32630"
            /note="Primer"
BASE COUNT 1 5 a 6 c 4 g 7 t
ORIGIN

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Query Match          74.3%; Score 10.4; DB 6; Length 22;
Best Local Similarity 84.6%; Pred. No. 2.8e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 CAGGTGTAGNCCA 14
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Db      18 CAGGTGTAGACCA 6

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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(Without alignments)
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Perfect score: 14

Sequence: 1 CCAGCTGTAGNCCA 14

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Maximum Match 100%

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SUMMARIES

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1	11.4	81.4	50	22	AAH90362	Human clone cg4398
2	11.4	81.4	50	22	AAH90364	Human clone cg4398
3	11	78.6	15	20	AAH90394	Tag sequence of a
4	11	78.6	15	24	ABK31947	Human colon cancer
5	11	78.6	31	22	AAI31182	Human single nucle
6	10.4	74.3	15	17	AAK65326	Mouse B7-1 hammet
7	10.4	74.3	15	17	AAK65327	Mouse B7-1 hammet
8	10.4	74.3	15	24	ABK52004	Human SLC18A2 alle
9	10.4	74.3	18	20	AAH84480	PCR primer for Hum

C	10	10.4	74.3	18	21	AAH52824	Human CD44 antisen
C	11	10.4	74.3	18	24	ABLA3601	Human chromosome 1
C	12	10.4	74.3	19	21	AAH58857	Oligonucleotide us
C	13	10.4	74.3	20	16	AAH01071	Mouse B7-1 (alt)en
C	14	10.4	74.3	20	19	AAH48029	Murine B7-1 target
C	15	10.4	74.3	20	21	AAH91878	Antisense primer t
C	16	10.4	74.3	20	22	AAH23148	Oligonucleotide fo
C	17	10.4	74.3	20	22	AAH32871	Murine B7-1 mRNA c
C	18	10.4	74.3	20	24	AAH34980	Human MTHFR gene c
C	19	10.4	74.3	20	24	AAH56640	Human MTHFR gene c
C	20	10.4	74.3	20	24	AAH56640	Human MTHFR gene c
C	21	10.4	74.3	20	24	AAH56640	Human MTHFR gene c
C	22	10.4	74.3	20	24	AAH56640	Human MTHFR gene c
C	23	10.4	74.3	21	17	AAH11220	Human chromosome 2
C	24	10.4	74.3	21	19	AAH21625	Human chromosome 2
C	25	10.4	74.3	21	19	AAH21625	Human chromosome 2
C	26	10.4	74.3	22	22	AAH50964	Human chromosome 2
C	27	10.4	74.3	22	22	AAH50964	Human chromosome 2
C	28	10.4	74.3	24	24	AAH34014	Human chromosome 2
C	29	10.4	74.3	25	20	AAH34310	Human chromosome 2
C	30	10.4	74.3	27	18	AAH55516	Human chromosome 2
C	31	10.4	74.3	27	18	AAH55516	Human chromosome 2
C	32	10.4	74.3	27	19	AAH55516	Human chromosome 2
C	33	10.4	74.3	29	24	AAH55516	Human chromosome 2
C	34	10.4	74.3	30	18	AAH55516	Human chromosome 2
C	35	10.4	74.3	31	22	AAH55516	Human chromosome 2
C	36	10.4	74.3	32	17	AAH55516	Human chromosome 2
C	37	10.4	74.3	32	17	AAH55516	Human chromosome 2
C	38	10.4	74.3	33	24	AAH55516	Human chromosome 2
C	39	10.4	74.3	37	19	AAH55516	Human chromosome 2
C	40	10.4	74.3	39	19	AAH55516	Human chromosome 2
C	41	10.4	74.3	45	16	AAH55516	Human chromosome 2
C	42	10.4	74.3	45	16	AAH55516	Human chromosome 2
C	43	10.4	74.3	45	20	AAH55516	Human chromosome 2
C	44	10.4	74.3	47	21	AAH55516	Human chromosome 2
C	45	10.4	74.3	47	20	AAH55516	Human chromosome 2

ALIGNMENTS

RESULT 1	AAH90362	standard; cDNA; 50 BP.
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AC	08-0CT-2001	(first entry)
DT	XX	
DE	Human clone cg43982025 SNP site, SEQ ID NO:242.	
XX	XX	
KW	Human: single nucleotide polymorphism; SNP; chromosome 19;	
KW	detection; identification; gene therapy; genetic disorder; ss.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FT	key	Location/Qualifiers
FT	variation	replace(25..26,GCC)
FT		/*tag=a
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PN	WO200147942-A2.	
XX	05-JUL-2001.	
PD	XX	
XX	27-DEC-2000; 2000WO-US53387.	
PF	XX	
XX	27-DEC-1999; 99US-0472865.	
PR	XX	
XX	(CURA-) CURAGEN CORP.	
PA	XX	
XX	Shimkets RA, Leach M;	
PI	XX	
XX	XX	

DR WPI; 2001-425617/45.

XX New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism.

PS Claim 1; Page 87; 295pp; English.

XX Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580
CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.

XX Sequence 50 BP; 9 A; 13 C; 21 G; 7 T; 0 other;

Query Match 81.4%; Score 11.4; DB 22; Length 50;

Best Local Similarity 85.7%; Pred. No. 3.6e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCCA 14

DB 19 CCAGGTGACAGGCCA 32

RESULT 2

AAH90364

ID AAH90364 standard; cDNA; 50 BP.

XX AAH90364;

DT 08-OCT-2001 (first entry)

DE Human clone c943982025 SNP site. SEQ ID NO:244.

XX Human; single nucleotide polymorphism; SNP; chromosome 19;

KW detection; identification; gene therapy; genetic disorder; ss.

XX Homo sapiens.

OS Key Location/Qualifiers
FH replace(25..26,CCA)
FT /*tag= a

XX /standard_name= "single nucleotide polymorphism"

PN WO200147942-A2.

PD 05-JUL-2001.

PF 27-DEC-2000; 2000MO-US5387.

PR 27-DEC-1999; 99US-0472865.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2001-425617/45.

XX New polynucleotides containing single nucleotide polymorphisms, for
PT detecting the presence of polymorphism, detecting a polymorphic site,
PT and treating a patient suffering from a pathology ascribed to the
PT polymorphism.

PS Claim 1; Page 87; 295pp; English.

XX Sequences AAH90121-AAH90700 represent 580 human cDNA sequences which
CC contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 568 (AAH90121-AAH90688) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 569 to 580 (AAH90689-AAH90700) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AAG64751-AAG64762). The SNPs
CC in sequences 569 to 574 (AAH90689-AAH90694) lead to conservative amino
CC acid changes, while those in sequences 575 to 578 (AAH90695-AAH90698)
CC result in non-conservative changes. The SNP in sequences 579 and 580
CC (AAH90699-AAH90700) generates a frameshift mutation. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic proteins/
CC peptides using the antibodies. The nucleic acids are useful for gene
CC therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.

XX Sequence 50 BP; 9 A; 13 C; 21 G; 7 T; 0 other;

Query Match 81.4%; Score 11.4; DB 22; Length 50;

Best Local Similarity 85.7%; Pred. No. 3.6e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCCA 14

DB 18 CCAGGTGACAGGCCA 31

RESULT 3

AAAX30994/c

ID AAAX30994 standard; DNA; 15 BP.

XX AAAX30994;

DT 21-MAY-1999 (first entry)

DE Tag sequence of a transcript increased in colorectal cancer.

XX Tag sequence; colorectal cancer; pancreatic cancer; colon cancer;

KW diagnosis; prognosis; treatment; ss.

XX Homo sapiens.

PN WO9853319-A2.

PD 26-NOV-1998.

PF 20-MAY-1998; 98MO-US10277.

PR 21-MAY-1997; 97US-0047352.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Kinzler KW, Vogelstein B;

DR WPI; 1999-070161/06.

PT Use of isolated gene transcripts - useful for developing products
PT for the diagnosis, prognosis and treatment of cancers, particularly
PT colon and pancreatic cancer

XX Claim 2; Page 24; 120pp; English.
PS
XX AAX30947-31815 represent tag sequences of transcripts that are
CC differentially expressed in colorectal cancer, in pancreatic
CC cancer, or in both. The tag sequences can be used to identify
CC genes by matching the tag to a gen data base member, or by using
CC the tag sequences as probes to isolate unidentified genes from
CC CDNA libraries. The tag sequences can also be used in a method
CC for diagnosing colon or pancreatic cancer in a sample suspected
CC of being neoplastic. The method comprises comparing the level of
CC at least one transcript in a first sample of a tissue to a second
CC sample, where the first sample is a colonic tissue suspected of
CC being neoplastic and the second sample is a normal human colonic
CC tissue. The transcript is identified by a tag selected from
CC AAX30947-31815. The methods of the invention can be used in the
CC diagnosis, prognosis and treatment of cancer.
XX
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;
Query Match 78.6%; Score 11; DB 20; Length 15;
Best Local Similarity, 91.7%; Pred. No. 5.8e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 AGGTGTAGNCCA 14
Db 14 AGGTGTAGCCCA 3
RESULT 4
ABK31947/c
ID ABK31947 standard; DNA: 15 BP.
AC ABK31947;
XX 23-APR-2002 (first entry)
DT
XX Human colon cancer SAGE tag #48.
DE
XX Human; colon cancer; colorectal cancer; pancreatic cancer; SAGE tag;
KM serial analysis of gene expression; diagnostic; prognostic; probe;
KW cancer marker; ss.
XX
XX Homo sapiens.
OS
XX US6333152-B1.
PN
XX 25-DEC-2001.
PD
XX 20-MAY-1998; 98US-0081646.
PF
XX 20-MAY-1998; 98US-0081646.
PR
XX 20-MAY-1998; 98US-0081646.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX Vogelstein B, Kinzler KW, Zhang L, Zhou W;
PI WPI; 2002-153821/20.
DR
XX New human nucleic acid containing specific SAGE tags, useful as
XX diagnostic markers for cancer, also derived probes
PT
XX
PS Disclosure; Column 15; 161pp; English.
XX
XX The invention relates to an isolated, purified human nucleic acid (1)
CC that has the same sequence as a mRNA found in humans and is a SAGE
CC (serial analysis of gene expression) tag comprising a single stranded
CC probe containing at least 10 consecutive nucleotides. SAGE tags, are
CC diagnostic and prognostic markers of cancer, especially of the colon and
CC pancreas. ABK31900-ABK32770 represent human colon and pancreatic cancer
CC SAGE tags of the invention.
XX
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 4 T; 0 other;

Query Match 78.6%; Score 11; DB 24; Length 15;
Best Local Similarity 91.7%; Pred. No. 5.8e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 AGGTGTAGNCCA 14
Db 14 AGGTGTAGCCCA 3
RESULT 5
AAI31182/c
ID AAI31182 standard; DNA: 31 BP.
XX
XX AAI31182;
AC
XX 18-OCT-2001 (first entry)
DT
XX Human single nucleotide polymorphism (SNP) 255.
DE
XX Human; resequence; genotype; disease; forensic; paternity testing;
KM single nucleotide polymorphism; SNP; ss.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH replace(16,T)
FT Variation /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX WO200166800-A2.
PD
XX 13-SEP-2001.
XX
XX 07-MAR-2001; 2001WO-US07268.
PF
XX 07-MAR-2000; 2000US-0187510.
PR
XX 22-MAY-2000; 2000US-0206129.
XX
XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA
XX Cargill M, Ireland JS, Lander ES;
PI WPI; 2001-522952/57.
DR
XX Nucleic acid molecules from the human genome which include polymorphic
XX sites, useful in methods for predicting the presence, absence or
XX severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype
XX
XX Claim 1; Page 132; 145pp; English.
PS
XX The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI3114) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
SQ Sequence 31 BP; 8 A; 8 C; 9 G; 6 T; 0 other;
Query Match 78.6%; Score 11; DB 22; Length 31;
Best Local Similarity 91.7%; Pred. No. 6e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CAGGTGTAGNCC 13
Db 14 CAGGTGTAGACC 3

RESULT 6
AA65326/c
ID AAX65326 standard; RNA; 15 BP.
XX
AC AAX65326;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1958.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN W09618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US15516.
XX
PR 05-OCT-1995; 95US-0541365.
PR 13-DEC-1994; 94US-0354920.
PR 23-DEC-1994; 94US-0363253.
PR 23-DEC-1994; 94US-0363254.
PR 17-FEB-1995; 95US-0390850.
PR 20-APR-1995; 95US-0426124.
PR 02-MAY-1995; 95US-0432874.
PR 04-MAY-1995; 95US-0434509.
PR 07-JUL-1995; 95US-0000951.
PR 07-JUL-1995; 95US-0000974.
PR 07-AUG-1995; 95US-0512861.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
PI Belgelman L, Karpelsky A, Modak A, Usman N, Burgin A;
PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used
PT for the treatment of arthritis, induction of graft tolerance or
PT treatment of auto-immune diseases
XX
PS Claim 10; Page 179; 307pp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
CC The ENA's can inhibit collagenase and stromelysin production in the
CC synovial membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly
CC specific. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 15 BP; 3 A; 4 C; 5 G; 3 U; 0 other;
XX
Query_Match 74.38; Score 10.4; DB 17; Length 15;
Best_Local_Similarity 84.68; Pred. No. 1.3e+04;

Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCAGGTGAGGCC 13
|||||||
Db 15 CCAGGTGAGTCC 3
RESULT 7
AA65327/c
ID AAX65327 standard; RNA; 15 BP.
XX
AC AAX65327;
XX
DT 20-JUL-1999 (first entry)
XX
DE Mouse B7-1 hammerhead ribozyme target SEQ ID NO:1959.
XX
KW Arthritic condition; graft tolerance; immune response; target; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; human; rabbit; mouse; collagenase;
KW stromelysin; synovial membrane; joint; arthritis; osteoarthritis;
KW rheumatoid arthritis; autoimmune disease; allergy; inflammation;
KW diagnosis; ss.
XX
OS Mus sp.
XX
PN W09618736-A2.
XX
PD 20-JUN-1996.
XX
PF 22-NOV-1995; 95WO-US15516.
XX
PR 05-OCT-1995; 95US-0541365.
PR 13-DEC-1994; 94US-0354920.
PR 23-DEC-1994; 94US-0363253.
PR 23-DEC-1994; 94US-0363254.
PR 17-FEB-1995; 95US-0390850.
PR 20-APR-1995; 95US-0426124.
PR 02-MAY-1995; 95US-0432874.
PR 04-MAY-1995; 95US-0434509.
PR 07-JUL-1995; 95US-0000951.
PR 07-JUL-1995; 95US-0000974.
PR 07-AUG-1995; 95US-0512861.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper K, Gustofson J, McSwiggen J, Pavco P, Stinchcomb DT;
PI Belgelman L, Karpelsky A, Modak A, Usman N, Burgin A;
PI Matulic-Adamic J, Jarvis T, Thompson JD, Wincott F;
XX
DR WPI; 1996-300653/30.
XX
PT Enzymatic nucleic acid molecules having a hammer-head motif - used
PT for the treatment of arthritis, induction of graft tolerance or
PT treatment of auto-immune diseases
XX
PS Claim 10; Page 179; 307pp; English.
XX
XX The present invention describes a novel enzymatic nucleic acid (ENA)
CC having a hammerhead motif (HM) comprising: (i) at least 5 ribose
CC residues; (ii) a 2'-C-allyl modification at position 4 of the ENA; (iii)
CC at least ten 2'-O-methyl modifications; and (iv) a 3'-end modification.
CC The ENA's can inhibit collagenase and stromelysin production in the
CC synovial membrane of joints for the treatment or prevention of arthritis,
CC particularly osteoarthritis or rheumatoid arthritis. The ENA's can also
CC be used to treat antigen presenting cells of a donor to induce tolerance
CC in a recipient to an alloantigen of a donor. They can also be used for
CC enhancing graft tolerance or for treating autoimmune disease, and for
CC treating allergies and other inflammatory conditions. The ENA's can also
CC be used in diagnosis. Ribozyme therapy impacts on the expression of
CC stromelysin without introducing the non-specific effects upon gene
CC expression which accompany treatment with retinoids and dexamethasone.
CC The concentration of ribozyme required to affect a therapeutic treatment
CC is lower than that required of antisense molecules, and is highly

CC specific. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 15 BP; 3 A; 4 C; 5 G; 3 U; 0 other;
XX
Query Match 74.3%; Score 10.4; DB 17; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCAGGTGTAGGCC 13
Db 14 CCAGGTGAGATCC 2
XX
RESULT 8
ABLS2004/C
ID ABL52004 standard; DNA; 15 BP.
XX
AC ABL52004;
XX
DT 11-JUL-2002 (first entry)
XX
DE Human SLC18A2 allele specific oligonucleotide primer SEQ ID NO:52.
XX
KW Human; solute carrier family 18 member 2; SLC18A2; vesicular monoamine;
KW vesicular monoamine transporter; VMAT2; polymorphic site; SNP;
KW single nucleotide polymorphism; antiinflammatory; neuroleptic;
KW haplotyping; genotyping; respiratory inflammatory disease;
KW neuropsychiatric disorder; monoaminergic brain system; primer; ss.
XX
OS Homo sapiens.
XX
FT Key Location/Qualifiers
FT misc_feature 14
FT /tag= a
FT /note= "polymorphic site indicated by an ambiguity base"
XX
PN WO200222652-A2.
XX
PD 21-MAR-2002.
XX
PF 17-SEP-2001; 2001WO-US42217.
XX
PR 15-SEP-2000; 2000US-232895P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Anastasio AE, Han J, Klem SE, Sausker EA;
XX
DR WPI; 2002-393942/42.
XX
PT Novel genetic variants of soluble carrier family 18 (vesicular
PT monoamine), member 2 gene useful for screening drugs to treat diseases
PT e.g. neuropsychiatric disorders involving monoaminergic brain systems
XX
PS Claim 17; Page 15; 183pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) having a
CC sequence (S1) comprising soluble carrier family 18 (vesicular monoamine),
CC member 2 (SLC18A2) isogene selected from 49 isogenes with regions of a
CC sequence (S2) of 40023 bp (see ABL51954), and defined by a corresponding
CC set of polymorphisms whose locations and identities are given in the
CC specification; or a sequence (S2) complementary to (S1). (I) has
CC antiinflammatory and neuroleptic activities, and can be used in gene
CC therapy. Methods from the present invention can be used for haplotyping
CC and genotyping the SLC18A2 gene in an individual. SLC18A2 is also known
CC as the vesicular monoamine transporter (VMAT2). (I) is useful in studying
CC the expression and function of SLC18A2, and in expressing the SLC18A2
CC protein for use in screening for candidate drugs to treat diseases
CC related to SLC18A2 activity and in studying the effect of the variation
CC on the biological activity of SLC18A2 as well as on the binding affinity
CC of candidate drugs targeting SLC18A2 for the treatment of respiratory

CC inflammatory diseases such as neuropsychiatric disorders involving
CC monoaminergic brain systems. The present sequence represents an allele
CC specific oligonucleotide (ASO) primer for human SLC18A2, which is given
CC in the present invention.
XX
SQ Sequence 15 BP; 2 A; 5 C; 4 G; 3 T; 1 other;
XX
Query Match 74.3%; Score 10.4; DB 24; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.3e+04;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 CAGGTGTAGGCCA 14
Db 13 CAGGTGTGGCCCA 1
XX
RESULT 9
AAAX84480
ID AAX84480 standard; DNA; 18 BP.
XX
AC AAX84480;
XX
DT 10-SEP-1999 (first entry)
XX
DE PCR primer for Human EDIRF II coding sequence.
XX
KW Embryo derived interleukin related factor; diagnosis; detection; therapy;
KW EDIRF-related disease; immune disorder; haematopoietic disorder;
KW developmental disorder; inflammatory disease; arthritis; psoriasis;
KW EDIRF II; PCR primer; ss.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO932632-A1.
XX
PD 01-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US27068.
XX
PR 19-DEC-1997; 97US-0994890.
XX
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
PI Holtzman DA;
XX
DR WPI; 1999-418929/35.
XX
PT Nucleic acid encoding embryo-derived interleukin-related factors
XX
PS Example 2; Page 75; 116pp; English.
XX
CC This sequence is a PCR primer for DNA encoding the embryo-derived
CC interleukin-related factor (EDIRF) of the invention, designated human
CC EDIRF II. The EDIRF DNA and protein sequences (and their homologues),
CC antibodies (Ab) specific for EDIRF, and other modulators are used:
CC (i) in screening and detection assays, e.g. for chromosome mapping,
CC tissue typing or forensic studies; (ii) in diagnosis, prognosis or
CC monitoring clinical trials; and (iii) for treating or preventing
CC EDIRF-related diseases (especially immune, haematopoietic,
CC differential, developmental or inflammatory disease, including
CC arthritis and psoriasis). The EDIRF coding sequence, or its fragments, are
CC also useful as probes and primers (for detecting related sequences and
CC disease-associated mutations, also for mutagenesis), for expressing
CC recombinant EDIRF and as source of antisense, ribozyme and peptide
CC nucleic acids (for inhibiting translation of EDIRF-derived mRNA. EDIRF is
CC used to raise Ab (useful for detecting EDIRF, including forms with
CC aberrant post-translational modification, for affinity purification and
CC therapeutically) and to screen for specific modulators (e.g. peptides or
CC peptidomimetics).
XX
SQ Sequence 18 BP; 4 A; 6 C; 6 G; 2 T; 0 other;

Query Match 74.3%; Score 10.4; DB 20; Length 18;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGGTGTAGNCCA 14
 ||||| ||||
 Db 3 CAGGTGCAGCCCA 15

RESULT 10
 AAA52824/C
 ID AAA52824 standard; DNA; 18 BP.

AC AAA52824;

DF 15-SEP-2000 (first entry)

XX Human CD44 antisense oligonucleotide ISIS# 18713.

DE Human: CD44; cell surface adhesion receptor; cytostatic; antirheumatic;
 KN antiinflammatory; antiarthritic; CD44 antisense inhibition;
 KM hyperproliferative disorder; cancer; inflammatory disorder;
 XX rheumatoid arthritis; ss.

OS Homo sapiens.

PN WO200035935-A1.

PD 22-JUN-2000.

PF 14-DEC-1999; 99WO-US29576.

PR 17-DEC-1998; 98US-0213719.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowser LM;

XX WPI: 2000-431564/37.

DR WPI: 2000-431564/37.

PT New antisense compound, that inhibits the expression of human cell
 surface adhesion receptor CD44, for treating hyperproliferative
 PT disorders and inflammatory conditions, such as cancer and rheumatoid
 arthritis -

XX Claim 3; Page 76; 105pp; English.

XX The present sequence is one of a large number of antisense
 CC oligonucleotides designed to target different regions of the human CD44
 CC mRNA. CD44 is a multifunctional human cell surface adhesion receptor.
 CC The oligonucleotides were analysed for effect on CD44 mRNA levels by
 CC quantitative real-time PCR analysis. Antisense oligonucleotides that
 CC inhibit CD44 expression can be used to treat CD44-associated conditions
 CC including hyperproliferative disorders, such as cancer, and inflammatory
 CC conditions, such as rheumatoid arthritis. The antisense compounds
 CC hybridise to CD44 nucleic acids, thus allowing sandwich and other assays
 CC to be easily constructed.

CC Note: The sequence has a phosphorothioate backbone and may be either an
 CC oligodeoxynucleotide or a chimeric oligonucleotide containing
 CC 2'-methoxyethyl (2'-MOE) wings and a deoxy gap. The ISIS number given
 CC above corresponds to the oligodeoxynucleotide sequence.

CC Sequence 18 BP; 6 A; 5 C; 4 G; 3 T; 0 other;

SO Query Match 74.3%; Score 10.4; DB 21; Length 18;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CAGGTGTAGNCCA 14
 ||||| ||||
 Db 16 CAGGTGTATCCA 4

RESULT 11
 ABL43601/C
 ID ABL43601 standard; DNA; 18 BP.

AC ABL43601;

DT 11-APR-2002 (first entry)

XX Human chromosome 1p36-35 PCR primer SEQ ID NO:645.

DE Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
 KM genome; PCR primer; ss.

OS Homo sapiens.

PN JP2001321190-A.

PD 20-NOV-2001.

PF 12-MAR-2001; 2001JP-0068285.

PR 10-MAR-2000; 2000JP-0066716.

PA (RIKA) RIKAKAKU KENKYUSHO.
 (GENO-) GENOTEX YG.

DR WPI: 2002-144136/19.

XX Arraying genome clones -

PT Claim 4; Page 17; 528pp; Japanese.

XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each well of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention.

XX Sequence 18 BP; 3 A; 5 C; 7 G; 3 T; 0 other;

SO Query Match 74.3%; Score 10.4; DB 24; Length 18;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 ||||| ||||
 Db 14 CCAGGTGCAGTCC 2

RESULT 12
 AAA58857/C
 ID AAA58857 standard; DNA; 19 BP.

AC AAA58857;

DT 20-OCT-2000 (first entry)

DE Oligonucleotide used for analysis and study of 2q breakpoint region.
 XX Tissue repair protein; orofacial clefting; wound healing;
 KW tissue repair; 2q breakpoint region; ss.
 XX
 OS Homo sapiens.
 XX
 PM WO200040719-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 06-JAN-2000; 2000WO-GB000003.
 XX
 PR 06-JAN-1999; 99GB-0000167.
 XX
 PA (UYLE-) UNIV LEEDS.
 XX
 PI Markham AF, Bonthron D;
 XX
 DR WPI: 2000-465983/40.
 XX
 XX New human and mouse nucleic acids encoding a tissue repair protein,
 PT useful for diagnosing and treating orofacial clefting, and for
 PT promoting wound healing and/or tissue repair -
 XX
 PS Disclosure: Page 44; 45pp; English.
 XX
 CC Oligonucleotides AA58825-58 were used in the analysis and study of
 CC the 2q breakpoint region, in the course of the invention to identify
 CC the gene encoding a tissue repair protein. Tissue repair gene
 CC polynucleotides are useful for determining expression of mRNA in
 CC selected target tissue, e.g. for diagnosing and treating orofacial
 CC clefting. They are also useful for determining the presence
 CC of DNA mutations in patients suffering from, or suspected to be
 CC suffering from orofacial clefting. The antibodies are also useful
 CC in the diagnosis of orofacial clefting. The polynucleotide is also
 CC useful for promoting wound healing and tissue repair.
 CC
 XX
 SQ Sequence 19 BP; 4 A; 7 C; 5 G; 3 T; 0 other:
 Query Match 74.3%; Score 10.4; DB 21; Length 19;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCAGGTGAGNCC 13
 ||||| ||||
 DB 13 CCAGGTGAGTCC 1
 RESULT 13
 AAT01071
 ID AAT01071 standard; DNA; 20 BP.
 XX
 AC AAT01071;
 XX
 DT 08-MAY-1996 (first entry)
 XX
 DE Mouse B7-1 (alternatively spliced form) PCR primer.
 XX
 KW T-cell costimulatory molecule; B7-2; T-lymphocyte; CD28; CTLA4;
 KW receptor; immunoglobulin; primer; polymerase chain reaction;
 KW PCR; ss.
 XX
 OS Synthetic.
 XX
 PM WO9523859-A2.
 XX
 PD 08-SEP-1995.
 XX
 PF 02-MAR-1995; 95WO-US02576.
 XX
 PR 02-MAR-1994; 94US-0205697.
 XX

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 PA (DAND) DANA FARBER CANCER INST.
 XX
 PI Borriello F, Freeman GJ, Nadler LM, Sharpe AH;
 XX
 DR WPI: 1995-320574/41.
 XX
 PT Novel T cell co-stimulatory molecules - corresponding to naturally
 PT occurring alternatively spliced forms of T cells co-stimulatory
 PT molecules or variants
 XX
 PS Example 7; Page 43; 11pp; English.
 XX
 CC RT-PCR was used to amplify mouse T-cell costimulatory molecule
 CC B7-1 cDNA fragments derived from murine spleen cell RNA. The
 CC primers used for primary PCR were a sense primer (AAT01068) and
 CC antisense primer (AAT01070), and for secondary PCR were a sense
 CC primer (AAT01069) and antisense primer (AAT01071). cDNA fragments
 CC were detected that encoded a B7-1 form in which the signal
 CC peptide domain was spliced directly to the Igc-1like domain,
 CC i.e. the Igv-1like domain was deleted (see AAR82900). Another cDNA
 CC fragment coded for a B7-1 form in which the Igv-1like domain was
 CC spliced directly to the transmembrane domain, i.e. the Igc-1like
 CC domain was deleted (see AAR82902).
 CC
 XX
 SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 other:
 Query Match 74.3%; Score 10.4; DB 16; Length 20;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCAGGTGAGNCC 13
 ||||| ||||
 DB 1 CCAGGTGAGTCC 13
 RESULT 14
 AAV48029
 ID AAV48029 standard; DNA; 20 BP.
 XX
 AC AAV48029;
 XX
 DT 19-OCT-1998 (first entry)
 XX
 DE Murine B7-1 targeted oligonucleotide 14914.
 XX
 KW ss; mouse; B7; T cell; inflammation; autoimmune disease; cell activation;
 KW cell proliferation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /note= "Phosphorochioate linkages"
 XX
 PM WO9829124-A1.
 XX
 PD 09-JUL-1998.
 XX
 PF 16-DEC-1997; 97WO-US23270.
 XX
 PR 31-DEC-1996; 96US-0777266.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Vickers TA;
 XX
 DR WPI: 1998-387783/73.
 XX
 PT New oligo:nucleotide(s) that modulate expression of B7 proteins -
 PT used for, e.g. controlling activation and proliferation of T cells,
 XX

PT particularly for treatment, diagnosis and prevention of inflammation
 XX Example 1; Page 36; 120pp; English.
 PS
 XX The oligonucleotides which specifically hybridise to B7 modulate its
 CC expression (and thus T cell activation and proliferation). This is
 CC particularly useful for treatment and prevention of inflammation and
 CC autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
 CC Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
 CC (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
 CC rhinitis, allergy, cancer and metastases. The oligonucleotides may also
 CC be used to manipulate T cell activation ex vivo; to determine or detect
 CC B7 protein expression; for diagnosis; as assay and purification reagents,
 CC and to study physiological roles of B7 proteins.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 other;

Query Match 74.3%; Score 10.4; DB 19; Length 20;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 ||||| 1 11
 Db 2 CCAGGTGAAGTCC 14

RESULT 15

AAA91878/c
 ID AAA91878 standard; DNA; 20 BP.

AC AAA91878;

DT 08-JAN-2001 (first entry)

DE Antisense primer to amplify bases 66 to 265 of human TGF b1 gene.

KW TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;
 human; primer; ss.

OS Homo sapiens.

PN WO200049169-A1.

PD 24-AUG-2000.

PF 18-FEB-2000; 2000WO-US04251.

PR 19-FEB-1999; 99US-0120787.

PA (DZGE-) DZGENES LLC.

PI Moskowitz DM;

DR WPI: 2000-549279/50.

PT Diagnosing genetic susceptibility for end-stage renal disease using
 PT single nucleotide polymorphisms, involves analyzing sample obtained
 PT from subject to detect genetic polymorphism in the sample
 PT polynucleotide -

PS Example 3; Page 36; 73pp; English.

CC The present invention relates the diagnosis of genetic susceptibility
 CC for end-stage renal disease (ESRD). The method involves analyzing a
 CC polynucleotide sample for a single nucleotide polymorphism (SNP)
 CC associated with an altered susceptibility for ESRD. The method allows
 CC early detection of ESRD and hence effective delay or ideally,
 CC prevention of ESRD is made possible. The present sequence is a primer
 CC used to amplify bases 66 to 265 of human TGF b1 gene. Polymorphisms
 CC the TGF b1 gene are known to be a probable trigger for renal apoptosis.

SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 other;

Query Match 74.3%; Score 10.4; DB 21; Length 20;
 Best Local Similarity 84.6%; Pred. No. 1.3e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CCAGGTGTAGNCC 13
 ||||| 1 11
 Db 15 CCAGGTGTAGTCC 3
 Search completed: June 21, 2003, 22:26:27
 Job time : 78.7812 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 16.625 seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-13
Perfect score: 14
Sequence: 1 CCAGGTGTAGNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/Backlist1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	78.6	15	US-09-081-646-48	Sequence 48, Appl
C 2	10.4	74.3	15	US-08-585-684B-820	Sequence 820, App
C 3	10.4	74.3	15	US-08-585-684B-821	Sequence 821, App
C 4	10.4	74.3	15	US-09-038-073-820	Sequence 820, App
C 5	10.4	74.3	15	US-09-038-073-821	Sequence 821, App
C 6	10.4	74.3	18	US-09-213-719-14	Sequence 14, Appl
C 7	10.4	74.3	20	US-08-777-266A-68	Sequence 68, Appl
C 8	10.4	74.3	20	US-08-205-697A-61	Sequence 61, Appl
C 9	10.4	74.3	20	US-08-702-525-61	Sequence 61, Appl
C 10	10.4	74.3	20	US-09-326-186B-68	Sequence 68, Appl
C 11	10.4	74.3	20	US-09-907-843-48	Sequence 48, Appl
C 12	10.4	74.3	20	PCT-US95-02576-61	Sequence 61, Appl
C 13	10.4	74.3	23	US-07-998-289B-26	Sequence 26, Appl
C 14	10.4	74.3	24	US-08-859-998-1077	Sequence 1077, App
C 15	10.4	74.3	24	US-08-765-332-4	Sequence 4, Appl
C 16	10.4	74.3	24	US-09-448-894-4	Sequence 4, Appl
C 17	10.4	74.3	24	US-09-225-928-1077	Sequence 1077, App
C 18	10.4	74.3	25	US-09-139-617-3	Sequence 3, Appl
C 19	10.4	74.3	25	US-09-139-617-15	Sequence 15, Appl
C 20	10.4	74.3	25	US-09-561-741A-3	Sequence 3, Appl
C 21	10.4	74.3	25	US-09-561-741A-15	Sequence 15, Appl
C 22	10.4	74.3	31	US-08-434-411-58	Sequence 58, Appl
C 23	10.4	74.3	31	US-08-434-402-58	Sequence 58, Appl
C 24	10.4	74.3	31	US-08-783-288-58	Sequence 58, Appl
C 25	10.4	74.3	31	US-08-890-640-58	Sequence 58, Appl
C 26	10.4	74.3	31	5194592-82	Patent No. 5194592
C 27	10.4	74.3	45	US-08-495-695B-25	Sequence 25, Appl

28	10.4	74.3	45	2	US-08-495-695B-26	Sequence 26, Appl
29	10.4	74.3	45	4	US-09-199-637A-123	Sequence 123, App
30	10.4	74.3	45	5	PCT-US94-14436-25	Sequence 25, Appl
31	10.4	74.3	45	5	PCT-US94-14436-26	Sequence 26, Appl
32	10	71.4	21	4	US-09-182-145-139	Sequence 139, App
33	10	71.4	23	2	US-08-129-151A-17	Sequence 17, Appl
34	10	71.4	23	2	US-08-715-579-17	Sequence 17, Appl
35	10	71.4	24	2	US-08-859-998-543	Sequence 543, App
36	10	71.4	24	4	US-09-225-928-543	Sequence 543, App
37	10	71.4	26	5	PCT-US92-06821A-25	Sequence 25, Appl
38	10	71.4	28	2	US-08-463-081B-19	Sequence 19, Appl
39	10	71.4	28	2	US-08-463-081B-20	Sequence 20, Appl
40	10	71.4	28	2	US-08-461-379A-19	Sequence 19, Appl
41	10	71.4	28	2	US-08-461-379A-20	Sequence 20, Appl
42	10	71.4	28	2	US-08-462-390B-19	Sequence 19, Appl
43	10	71.4	28	2	US-08-462-390B-20	Sequence 20, Appl
44	10	71.4	28	3	US-08-833-963C-4	Sequence 4, Appl
45	10	71.4	28	3	US-08-463-074B-19	Sequence 19, Appl

ALIGNMENTS

```

RESULT 1
US-09-081-646-48/c
: Sequence 48, Application US/09081646
: Patent No. 6333152
:
: GENERAL INFORMATION:
: APPLICANT: Kinzler, Kenneth
: APPLICANT: Vogelstein, Bert
: APPLICANT: Zhang, Lin
: APPLICANT: Zhou, Wei
:
: TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
: FILE REFERENCE: 01107.74664
: CURRENT FILING DATE: 1998-05-20
: EARLIER APPLICATION NUMBER: 60/047,352
: EARLIER FILING DATE: 1997-05-21
: NUMBER OF SEQ ID NOS: 871
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 48
: LENGTH: 15
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-081-646-48

Query Match          78.6%  Score 11; DB 4; Length 15;
Best Local Similarity 91.7%  Pred. No. 6.6e+02;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 AGGTGTAGNCCA 14
Db      14 AGGTGTAGNCCA 3
|||||||
|

RESULT 2
US-08-585-684B-820/c
: Sequence 820, Application US/08585684B
: Patent No. 5877021
:
: GENERAL INFORMATION:
: APPLICANT: Stinchcomb, Daniel T.
: APPLICANT: Jarvis, Thale
: APPLICANT: McSwiggen, James
:
: TITLE OF INVENTION: METHOD AND REAGENT FOR THE
: TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
: NUMBER OF SEQUENCES: 2751
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles

```

```

1      STATE: California
2      COUNTRY: u.s.a.
3      ZIP: 90071
4
5      COMPUTER READABLE FORM:
6      MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
7      MEDIUM TYPE: Storage
8      COMPUTER: IBM Compatible
9      OPERATING SYSTEM: IBM P.C. DOS 5.0
10     SOFTWARE: FastSeq Version 1.15
11
12     CURRENT APPLICATION DATA:
13     APPLICATION NUMBER: US/08/585,684B
14     FILING DATE: January 16, 1996
15     PRIOR APPLICATION DATA:
16     APPLICATION NUMBER: 60/000,951
17     FILING DATE: July 7, 1995
18
19     ATTORNEY/AGENT INFORMATION:
20     NAME: Warburg, Richard
21     REGISTRATION NUMBER: 32,327
22     REFERENCE/DOCKET NUMBER: 218/078
23
24     TELECOMMUNICATION INFORMATION:
25     TELEPHONE: (213) 489-1600.
26     TELEFAX: (213) 955-0440
27     TELEX: 67-3510
28
29     INFORMATION FOR SEQ. ID NO.: 820:
30     SEQUENCE CHARACTERISTICS:
31     LENGTH: 15 base pairs
32     TYPE: nucleic acid
33     STRANDEDNESS: single
34     TOPOLOGY: linear
35
36     US-08-585-684B-820

```

Query Match	74.3%	Score 10.4	DB 2	Length 15
Best Local Similarity	84.6%	Pred. No. 1.5e+03		
Matches 11	Conservative 0	Mismatches 2	Indels 0	Gaps 0

```
Q7      1 CCAGGTGTAGNCC 1
          |||||  ||
Db     15 CCAGGTGAAGTCC 3
```

RESULT 3
US-08-585-684B-821/C
; Sequence 821, Application US/08585684B
; Patent No. 5877021

:
:
: APPLICANT: Stinchcomb, Daniel T.
:
: APPLICANT: Jarvis, Thale
:
: APPLICANT: McSwiggen, James
:
: TITLE OF INVENTION: METHOD AND REAGENT FOR THE
:
: TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
:
: TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
:
: NUMBER OF SEQUENCES: 2751
:
: CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.

```

; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDICAL RECORDS

```

```

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBMCompatiblc

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CONTROL:  IBM COMPATIBLE
OPERATING SYSTEM:  IBM P.C. DOS 5.0
SOFTWARE:  FastSEO Version 1.5

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CURRENT APPLICATION DATA:
APPLICATION NUMBER:  US/08/585,684B

```

;; FILING DATE: January 16, 1996
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000
FILING DATE: July 7, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/07B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 821:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-565-684B-821

Query Match	74.3%	Score 10.4;	DB 2;	Length 15;
Best Local Similarity	84.6%	Pred. No. 1.5e+03;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	CCAGGTGTAGNCC	1
Db	14	CCAGGTGAAGTCC	2

RESULT 4
US-09-038-073-820/c
; Sequence 820, Application US/09038073

```

; Patent NO. 6194150
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T
; ADDRESSEE: Jarvis, Walter

```

1
 2 APPLICANT: McSwiggen, James
 3
 4 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 5
 6 TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
 7
 8 TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
 9
 10 NUMBER OF SEQUENCES: 2751

;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ;

ZIP: 90071

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: 5.25" Diskette, 1.44 Mb

```

```

; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM PC DOS 5.0

```

```

/ OPERATING SYSTEM: IBM F.C. DOS 3.1
;
; SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/038,073
FILING DATE:

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,684
;

```

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:

```

; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE / DOCKET NUMBER: 310,070

```

REFERENCE/DOCKET NUMBER: 218/0/8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510

```

; INFORMATION FOR SEQ ID NO: 820:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 15 base pair
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; 00 000 000 000

```

US-09-038-0/3-820

Query Match	74.38;	Score 10.4;	DB 4;	Length 15;
-------------	--------	-------------	-------	------------

Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13
Db 15 CCAGGTGAGTCC 3

RESULT 5

US-09-038-073-821/C
Sequence 821, Application US/09038073
Patent No. 6194150

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Daniel T.
APPLICANT: Jarvis, Thale
APPLICANT: McSwigen, James

TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE

TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
NUMBER OF SEQUENCES: 2751

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: California

COUNTRY: U.S.A.
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/038,073
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,684

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 218/078
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 821:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-09-038-073-821

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 4; Length 15;
Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13
Db 14 CCAGGTGAGTCC 2

RESULT 6

US-09-213-719-14/C
Sequence 14, Application US/09213719B
Patent No. 6150162

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowart

TITLE OF INVENTION: ANTISENSE MODULATION OF CD44 EXPRESSION

FILE REFERENCE: RTS-0006
CURRENT APPLICATION NUMBER: US/09/213,719B
CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 91
SEQ ID NO 14

LENGTH: 18
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Antisense Oligonucleotide
US-09-213-719-14

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 3; Length 18;
Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAGGTGTAGNCCA 14
Db 16 CAGGTGATGCCA 4

RESULT 7

US-08-777-266A-68
Sequence 68, Application US/08777266A
Patent No. 6077833

GENERAL INFORMATION:

APPLICANT: Clarence Frank Bennett
APPLICANT: Timothy A. Vickers

TITLE OF INVENTION: Oligonucleotide Compositions and
TITLE OF INVENTION: Methods for the Modulation of the Expression of B7 proteins

NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 210 Lake Drive East, Suite 201

CITY: Cherry Hill
STATE: NJ

COUNTRY: USA
ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,266A

FILING DATE: December 31, 1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: ISPH-0201
TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:

LENGTH: 20
TYPE: Nucleic Acid

STRANDEDNESS: Single
TOPOLOGY: linear

ANTI-SENSE: Yes
US-08-777-266A-68

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 3; Length 20;
Matches 11: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13
Db 2 CCAGGTGAGTCC 14

RESULT 8

US-08-205-697A-61
; Sequence 61, Application US/08205697A
; Patent No. 6218510

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon J.

; TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/205,697A

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BWI-120

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

US-08-205-697A-61

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 4; Length 20;
Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 1 CCAGGTGAGTCC 13

RESULT 9

US-08-702-525-61
; Sequence 61, Application US/08702525
; Patent No. 6294660

; GENERAL INFORMATION:

; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon J.

; APPLICANT: Nadler, Lee W.

; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory

; TITLE OF INVENTION: Molecules and Uses Therefor

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,525

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/205,697

FILING DATE: 02-Mar-1994

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: BWI-120CPUS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: oligonucleotide

US-08-702-525-61

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 4; Length 20;
Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 1 CCAGGTGAGTCC 13

RESULT 10

US-09-326-186B-68
; Sequence 68, Application US/09326186B
; Patent No. 6319906

; GENERAL INFORMATION:

; APPLICANT: Bennett, Clarence Frank

; APPLICANT: Vickers, Timothy A.

; TITLE OF INVENTION: Oligonucleotide Compositions and Methods for the

; TITLE OF INVENTION: Modulation of the Expression of B7 Protein

; FILE REFERENCE: ISPH-0376

; CURRENT APPLICATION NUMBER: US/09/326,186B

; PRIOR FILING DATE: 1999-06-04

; PRIOR APPLICATION NUMBER: 08/777,266

; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-09-326-186B-68

Query Match

Best Local Similarity 74.3%; Score 10.4; DB 4; Length 20;
Pred. No. 1.5e+03;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCC 13

Db 2 CCAGGTGAGTCC 14

RESULT 11

US-09-907-843-48/C
; Sequence 48, Application US/09907843
; Patent No. 6440739

STREET: 2200 Sand Hill Road, suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1077:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1077

Query Match 74.3%; Score 10.4; DB 2; Length 24;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNC 13
DB 1 CCAGGTGTAGCTC 13

RESULT 15
US-08-765-332-4
Sequence 4, Application US/08765332
Patent No. 6025132
GENERAL INFORMATION:
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
APPLICANT: VAN HEUVERSWYN, HUGO
TITLE OF INVENTION: SIMULTANEOUS DETECTION, IDENTIFICATION
TITLE OF INVENTION: AND DIFFERENTIATION OF EUBACTERIAL TAXA USING A
NUMBER OF SEQUENCES: 216
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,332
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/02452
FILING DATE: 23-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870032.0
FILING DATE: 07-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870106.5
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-765-332-4

Query Match 74.3%; Score 10.4; DB 3; Length 24;
Best Local Similarity 84.6%; Pred. No. 1.5e+03;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNC 13
DB 9 CCAGGTGTAGTCC 21

Search completed: June 22, 2003, 00:01:36
Job time: 18.625 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.734 seconds
(without alignments)
374.936 Million cell updates/sec

Title: US-09-964-666-13

Perfect score: 14

Sequence: 1 CCACGTGTAGNCCA 14

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estiro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	78.6	41	17	AL766269 Arabidops
2	10.4	74.3	37	17	AZ850196 2M0151P19
3	10.4	74.3	37	17	BH129921 G-6C8.fM
4	10.4	74.3	38	10	BE534187 601232196
5	10.4	74.3	41	10	AV832412 AV832412
6	10.4	74.3	48	13	BI154032 602871096

Result No.	Score	Query Match	Length	ID	Description
7	10.4	74.3	49	12	BE739587 60156558
8	10	71.4	28	14	R63848 y121a09.f1
9	10	71.4	31	17	A2346490 1M0081004
10	10	71.4	43	17	A2832832 2M0113D06
11	10	71.4	46	9	AA677571 zj66f03.s
12	9.8	70.0	28	9	AA510334 vg32c11.f
13	9.8	70.0	31	13	BI259862 602971524
14	9.8	70.0	42	17	BH791916 SALR_0619
15	9.8	70.0	44	17	A2579484 1M0241M16
16	9.8	70.0	45	17	A2445734 1M0241M16
17	9.8	70.0	46	9	AA127131 z187e01.f
18	9.8	70.0	48	14	C21079 HUMG5000359
19	9.8	70.0	49	14	T93720 y609g01.f1
20	9.8	70.0	50	9	AU105239 AU105239
21	9.8	70.0	50	9	AU107231 AU107231
22	9.8	70.0	50	13	BM182676 fv60f03.y
23	9.8	70.0	50	14	N34794 y116g04.s1
24	9.4	67.1	25	17	A2864400 2M0173P24
25	9.4	67.1	27	17	A2772618 1M0583H09
26	9.4	67.1	33	17	A2585484 1M0390M07
27	9.4	67.1	33	17	AL766826 Arabidops
28	9.4	67.1	34	17	A2581060 1M0369C05
29	9.4	67.1	36	17	A2461229 1M0267F04
30	9.4	67.1	37	17	A2601449 1M0419A16
31	9.4	67.1	39	17	A2875800 2M0190C04
32	9.4	67.1	40	9	AA991123 BSBMFE520
33	9.4	67.1	43	9	AA910920 0K87N09.S
34	9.4	67.1	43	17	A2872071 2M0185E13
35	9.4	67.1	47	17	A2628215 1M0480M07
36	9.4	67.1	49	9	A1719563 as54d09.x
37	9.4	67.1	49	14	T68434 yC42d01.s1
38	9.4	67.1	49	17	A2470802 1M0285N10
39	9.4	67.1	50	9	AU104849 AU104849
40	9.4	67.1	50	17	BH233070 100617ID0
41	9.4	67.1	22	9	A1219622 9910d07.x
42	9.4	67.1	29	17	A2491277 1M0324E14
43	9.4	67.1	29	17	TA97A010 AL64465 T. brucei
44	9.4	67.1	30	17	A2924604 490611c29
45	9.4	67.1	31	17	A2492224 1M0326B13

ALIGNMENTS

RESULT 1
AL766269/c 41 bp DNA linear GSS 18-JUN-2002
Arabidopsis thaliana T-DNA flanking sequence GK-209A10-014557,
genomic survey sequence.
AL766269
AL766269.1 GI:21519402
GSS.
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H.
and Weisshaar,B.
A pipeline for automated high-throughput generation of FSTS
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 41)
Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

COMMENT

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f2611. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. 41
Location/Qualifiers
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-209A10-014557"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT

8 a 12 c 9 g 12 t

ORIGIN

Query Match 78.6%; Score 11; DB 17; Length 41;
Best Local Similarity 91.7%; Pred. No. 3.1e+04;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 3 AGGTGTAGNCCA 14
|||||
30 AGGTGTAGCCCA 19

Db 30 AGGTGTAGCCCA 19

RESULT 2

A2850196

LOCUS

DEFINITION 2M0151P19R Mouse 10kb plasmid UUGCLM library Mus musculus genomic

ACCESSION A2850196 37 bp DNA linear GSS 21-FEB-2001

VERSION A2850196.1 GI:13034963

KEYWORDS

SOURCE

ORGANISM

house mouse.

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 37)
Dunn,D., Aoyagi,A., Barber,M., Beacon,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0151 row: P column: 19
Seq primer: CACACAGCAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers
1. 37
/organism="Mus musculus"
/strain="C57BL/6J"

FEATURES

source

BASE COUNT

8 a 7 c 12 g 10 t

ORIGIN

Query Match 74.3%; Score 10.4; DB 17; Length 37;
Best Local Similarity 84.6%; Pred. No. 6.7e+04;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCAGGTGTAGNCC 13
|||||
23 CCAGGTGTAGCAC 35

Db 23 CCAGGTGTAGCAC 35

RESULT 3

BH129921

LOCUS

DEFINITION G-6c8.f Maize Random Small-insert Genomic Library Zea mays genomic

ACCESSION BH129921 37 bp DNA linear GSS 23-JUL-2001

VERSION BH129921.1 GI:14998762

KEYWORDS

SOURCE

ORGANISM

Zea mays.

Zea mays

REFERENCE

AUTHORS

1 (bases 1 to 37)
Meyers,B.C., Tingey,S.V. and Morgante,M.
Abundance, distribution and transcriptional activity of repetitive elements in the maize genome
Genome Res. 11 (10), 1660-1676 (2001)

TITLE

JOURNAL

COMMENT

Medline
Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases: forward and reverse reads were assembled when significant overlaps were detected.
Seq primer: M13univ
Class: shotgun.
Location/Qualifiers
1. 37
/organism="Zea mays"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-6c8"

FEATURES

source

```

/clone_lib="Maize Random Small-insert Genomic Library"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="young leaf"
/dev_stage="seedling"
/note="Vector: PCR-Script; Total genomic DNA was nebulized
; ends were polished with Pfu polymerase and the fragments
cloned into PCR-Script."
BASE COUNT      6 a      12 c      11 g      4 t      4 others
ORIGIN

```

Query Match	74.3%	Score 10.4	DB 17	Length 37
Best Local Similarity	84.6%	Pred No. 6	7e+04	
Matches 11	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	1	CCAGGTGTAGNCC	13
	11	1111111111	
Db	12	CCGGGTGTAGCCC	24

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 38)	NIH-MGC	http://mgc.nhl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strassberg, Ph.D.			

```

FEATURES
source
1. .38
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M6772 row: p column: 23
High quality sequence stop: 38.
Location/Qualifiers
1. .38

```

```

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3596038"
/clone_1b="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: Saliv
Site_2: Noli; Cloned unidirectionally. Primer: Oligo dT
library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

```

Query Match	Score 10.4	DB 10	Length 38
Best Local Similarity	74.3%	Pred. No. 6.7e+04	
Matches 11: Conservative	0: Mismatches 2:	Indels 0:	Gaps 0
07	1 CCAGGTGTAGMCC	13	
		11	
db	15 CCAGGTGGAGGCC	27	

RESULT	5	
AV832412/c		
LOCUS		
DEFINITION	AV832412 K. Sato unpublished cdna library: Hordeum vulgare subsp.	
	41 bp	mRNA linear EST 22-JUN-2001

LOCUS	AV832412	41 bp	mRNA	linear	EST 22-JUN-2001
DEFINITION	AV832412 K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA clone baak12ml8, mRNA sequence.				
ACCESSION	AV832412				

ACCESSION	AV832412
VERSION	AV832412.1
REVISION	GI:14524501
ECM	

SOURCE: *Hordeum vulgare* subsp. *vulgare*

Candidium variegale subsp. variegale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Gymnosperms; Magnoliopsida; Fabales; Leguminosae; Papilionaceae; Aeschynomene

REFERENCE
1 (bases 1 to 41)
; Triticaceae; Hordeum.
Triticaceae; Hordeum;
Spermatophyta; Magnoliopsida; Liliaceae;
Liliaceae

1 (bases 1 to 41)
Sato, K.
Relevance of communication research in WFO and Chinese National

Unpublished (2001)
Contact: Kazuhiro Sato

Research Institute for Bioreactors
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0045, Japan
Email: kazuo@rdb.okayama-u.ac.jp,
URL: <http://www.rdb.okayama-u.ac.jp/barley/>
Sato, K., Saitoh, K., Takeeda, K., Shini, T. and Kohara, Y. Direct
submission:
database: <http://www.shigen.nig.ac.jp/barley/Barley.html>

FEATURES	Location/Qualifiers
source	1. .41

```

/organism="Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref="taxon:112509"
/clone="baak12m18"
/clone_1b="K. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare leaves vegetative stage"
/tissue_type="leaves"
/dev_stage="vegetative stage"
7 a 9 c 18 g 7 l
BASE COUNT
ORIGIN

```

Query Match	74.3%	Score 10.4	DB 10	Length 41
Best Local Similarity	84.6%	Pred. No. 6.9e+04		
Matches 11	Conservative 0	Mismatches 2	Indels 0	Gaps 0

QY	1	CCAGGTGTAGNCC	13
Db	27	CCAGGTGAAGTCC	15

RESULT	6				
LOCUS	BI154032/c				
DEFINITION	BI154032	48 bp	mRNA	linear	EST_05-JUL-2001
ACCESSION	602871096F2	NCI_CGAP_Mam2	Mus musculus	CDNA clone	IMAGE:5003014 5'
VERSION	BI154032				
KEYWORDS	BI154032.1	GI:14614033			
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				

REFERENCE	1 (bases 1 to 48)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLAM1038 row: P column: 23
 High quality sequence stop: 44.
 Location/Qualifiers

FEATURES

source

1.48
 /organism="Mus musculus"
 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:5003014"
 /clone_lib="NCL_CGAP_Mam2"
 /tissue_type="tumor, diopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site:1; Salt:
 Site:2; NotI: Cloned unidirectionally. Primer: Oligo dt.
 library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"
 9 a 10 c 23 g 6 t

BASE COUNT

ORIGIN

Query Match 74.3%; Score 10.4; DB 13; Length 48;
 Best local Similarity 84.6%; Pred. No. 7.2e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 1111111111
 Db 41 CCAGGAGTAGGCC 29

RESULT 7
 BE739587 49 bp mRNA linear EST 15-SEP-2000
 LOCUS 6015655871 NIH_MGC_58 Homo sapiens CDNA clone IMAGE:3826142.3',
 DEFINITION mRNA sequence.

ACCESSION BE739587
 VERSION BE739587.1 GI:10153579
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 49)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgephs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONETECH Laboratories, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHC493 row: d column: 15
 High quality sequence start: 33
 High quality sequence stop: 49.
 Location/Qualifiers

FEATURES

source

1.49
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3826142"
 /clone_lib="NIH_MGC_58"
 /tissue_type="hypermethroma"
 /lab_host="DH10B (T1 phase-resistant)"
 /note="Organ: kidney; Vector: pMR-LIB (Clontech); Site:1;
 Site:2; NotI: Cloned unidirectionally. Primer: Oligo dt.
 Double-stranded CDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CAGCGCCATATGACC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCGCGGACACATG-dt(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T).
 Average

Insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA).
 7 a 21 c 12 g 9 t

BASE COUNT

ORIGIN

Query Match 74.3%; Score 10.4; DB 12; Length 49;
 Best local Similarity 84.6%; Pred. No. 7.2e+04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCAGGTGTAGNCC 13
 1111111111
 Db 17 CCAGGTGAGGCC 5

RESULT 8
 R63848 28 bp mRNA linear EST 26-MAY-1995
 LOCUS Y121a09.r1 Soares placenta Nb2HP Homo sapiens CDNA clone
 DEFINITION IMAGE:139864.5' similar to SP:TSC2_MOUSE Q00992 PUTATIVE REGULATORY
 PROTEIN ;, mRNA sequence.

ACCESSION R63848
 VERSION R63848.1 GI:835727
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 28)
 AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,R., Hawkin,M., Holman
 M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston
 R., Williamson,A., Woldmann,P. and Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)
 JOURNAL Contact: Willson RK
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence starts: 1
 High quality sequence stops: 1
 Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: M13RP1
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1.28
 /organism="Homo sapiens"
 /db_xref="GDB:550462"
 /db_xref="taxon:9606"
 /clone="IMAGE:139864"
 /clone_lib="Soares placenta Nb2HP"
 /sex="female"
 /dev_stage="placenta obtained at birth (full term)"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: pRT3D (Pharmacia) with a
 modified polylinker; Site:1; Not I; Site:2; Eco RI; 1st
 strand CDNA was primed with a Not I - oligo(dT) primer [5'
 AACTGGAAGATTCGCGCCGAGGAGATTTTCTTTTCTTTT 3']
 double-stranded CDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT73 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M. Fatima Bonaldo.
 8 a 6 c 8 g 6 t

BASE COUNT

ORIGIN

Query Match 71.4%; Score 10; DB 14; Length 28;
 Best Local Similarity 90.9%; Pred. No. 1e+05;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGCTAGNCCA 14
 1111111111
 Db 12 GGCTAGACCA 22

RESULT 9

A2346490/c

LOCUS 31 bp DNA linear GSS 29-SEP-2000

DEFINITION 1M0081004R Mouse 10kb plasmid UUGCJM library Mus musculus genomic

clone UUGCJM0081004 R, DNA sequence.

A2346490

ACCESSION A2346490.1 GI:10425727

VERSION GSS.

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 31)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: 0 column: 04

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 31.

Location/Qualifiers

1. 31

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGCJM0081004"

/clone_lib="Mouse 10kb plasmid UUGCJM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g114732114gb1A129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance.

BASE COUNT 7 a 11 c 5 g 8 t

ORIGIN

Query Match 71.4%; Score 10; DB 17; Length 31;
 Best Local Similarity 90.9%; Pred. No. 1.1e+05;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 CAGCTGAGNC 12
 1111111111
 Db 23 CAGCTGAGTC 13

RESULT 10

A2832832/c

LOCUS 43 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0113D06R Mouse 10kb plasmid UUGCJM library Mus musculus genomic

clone UUGC2M0113D06 R, DNA sequence.

A2832832

ACCESSION A2832832.1 GI:13002740

VERSION GSS.

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 43)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0113 row: D column: 06

Seq primer: CACACAGGAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 43.

Location/Qualifiers

1. 43

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0113D06"

/clone_lib="Mouse 10kb plasmid UUGCJM library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (g114732114gb1A129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance.

BASE COUNT 15 a 9 c 11 g 8 t

ORIGIN

mRNA sequence.
 BI259862
 BI259862.1 GI:14817604
 EST.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 31)
 NIH-MGC <http://mgc.ncl.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
 plate: L1AM1269 row: O column: 05
 high quality sequence stop: 31.
 Location/Qualifiers
 1. 31
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5111260"
 /clone_1lb="NIH_MGC_12"
 /tissue_type="cervical carcinoma cell line"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NOTI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 Technology: 1.4 kb. Library prepared by Life
 Technologies."

BASE COUNT
 3 a 12 c 6 g 10 t

ORIGIN
 Query Match 70.0%; Score 9.8; DB 13; Length 31;
 Best Local Similarity 78.6%; Pred. No. 1.4e+05;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14
 11111 11111
 Db 23 CCAGAGAGAGGCCA 10

RESULT 14
 BH791916
 LOCUS
 DEFINITION
 SALK_061994.25.20 x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_061994.25.20.x, DNA
 sequence.
 ACCESION
 BH791916
 VERSION
 BH791916.1 GI:19886386
 KEYWORDS
 GSS.
 SOURCE
 ORGANISM
 Arabidopsis thaliana
 thale cress.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 42)
 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriub
 ,C., Jaske,A., Karnes,M., Kim,C.J., Parker,H., Prediis,L., Shinn,P.
 , Zimmerman,J. and Ecker,J.R.
 A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752

TITLE
 JOURNAL
 COMMENT

Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA. This sequence lies within 300 bases of the 5' end of
 AT2929210.
 Class: TDNA tagged.
 Location/Qualifiers
 1. 42
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_061994.25.20.x"
 /clone_1lb="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT
 11 a 11 c 6 g 14 t

ORIGIN
 Query Match 70.0%; Score 9.8; DB 17; Length 42;
 Best Local Similarity 78.6%; Pred. No. 1.5e+05;
 Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCAGGTGTAGNCCA 14
 11111 11111
 Db 8 CCAGTTTACGCCA 21

RESULT 15
 A2579484/c
 LOCUS
 DEFINITION
 A2579484 44 bp DNA linear GSS 13-DEC-2000
 1M0367B06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0367B06 F, DNA sequence.
 A2579484
 A2579484.1 GI:11693913
 GSS.
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 44)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Petersen,T., Rellily
 ,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhauser,A.
 and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0367 row: B column: 06
 Seq primer: CGTTGTAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 44.
 Location/Qualifiers
 1. 44
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0367B06"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

TITLE
 JOURNAL
 COMMENT

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 9 a 11 c 13 g 11 t
ORIGIN

Query Match 70.0%; Score 9.8; DB 17; Length 44;
Best Local Similarity 78.6%; Pred. No. 1.5e+05;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCAGTGTAGNCCA 14
||||| 11
Db 18 CCAGATGTAGACGA 5

Search completed: June 21, 2003, 23:59:07
Job time: 610.901 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 281.094 Seconds
(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-14

Sequence: 1 CAAGTCACAGNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_or:*

21: em_ov:*

22: em_pat:*

23: em_ph:*

24: em_pl:*

25: em_ro:*

26: em_sts:*

27: em_un:*

28: em_vl:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_in:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vit:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	24	6	AX443826
C 2	12	85.7	25	6	AX447806
C 3	11.4	81.4	17	6	AR006801
C 4	11.4	81.4	17	6	AR008981
C 5	11.4	81.4	17	6	AR135409
C 6	11.4	81.4	17	6	161180
C 7	11.4	81.4	17	6	171313
C 8	11.4	81.4	17	6	178729
C 9	11.4	81.4	18	6	AX250348
C 10	11.4	81.4	22	6	AR103422
C 11	11.4	81.4	22	6	AR151630
C 12	11.4	81.4	24	6	AX350160
C 13	11.4	81.4	26	6	AR006770
C 14	11.4	81.4	26	6	AR135378
C 15	11.4	81.4	26	6	171282
C 16	11.4	81.4	27	6	A40952
C 17	11.4	81.4	27	6	A44325
C 18	11.4	81.4	27	6	A80258
C 19	11.4	81.4	27	6	AR076531
C 20	11.4	81.4	27	6	E38897
C 21	11.4	81.4	29	6	BD013342
C 22	11.4	81.4	29	23	BD010299
C 23	11.4	81.4	30	6	AR067963
C 24	11.4	81.4	30	6	AR078918
C 25	11.4	81.4	30	6	AR097712
C 26	11.4	81.4	32	6	E10691
C 27	11.4	81.4	34	6	E40701
C 28	11.4	81.4	38	6	AR096917
C 29	11.4	81.4	38	6	AX467501
C 30	11.4	81.4	38	6	112040
C 31	11.4	81.4	39	6	AX374843
C 32	11.4	81.4	39	6	AX467500
C 33	11.4	81.4	46	6	AR035242
C 34	11	78.6	23	6	AX306373
C 35	11	78.6	23	6	AX320086
C 36	11	78.6	23	6	AX352397
C 37	11	78.6	23	6	AX419617
C 38	10.6	75.7	21	6	AX095382
C 39	10.6	75.7	31	6	AX248084
C 40	10.4	74.3	19	6	AR180271
C 41	10.4	74.3	15	6	AX131418
C 42	10.4	74.3	20	6	AX296985
C 43	10.4	74.3	20	6	AX370507
C 44	10.4	74.3	20	6	E35314
C 45	10.4	74.3	20	6	E35315

ALIGNMENTS

RESULT 1

AX443826/c

LOCUS AX443826 24 bp DNA

DEFINITION Sequence 281 from Patent WO0216649.

ACCESSION AX443826

VERSION AX443826.1 GI:21691104

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

synthetic construct

artificial sequences.

REFERENCE

1

AUTHORS Gunderson, K.

TITLE Probes and decoder oligonucleotides

JOURNAL Patent: WO 0216649-A 281 28-FEB-2002;

Illumina, Inc. (US)

FEATURES
source
Location/Qualifiers
1. .24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

BASE COUNT
5 a 5 c 8 g 6 t

ORIGIN

Query Match
Best Local Similarity 85.7%; Score 12; DB 6; Length 24;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 CAAGTCCAGNCC 13
19 CAAGTCCAGACC 7

Db

RESULT 2
AX447806 25 bp DNA Linear PAT 03-JUL-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Gunderson, K.
TITLE
Probes and decoder oligonucleotides
JOURNAL
Patent: WO 0216649-A 4261 28-FEB-2002;
Illumina, Inc. (US)
Location/Qualifiers

FEATURES
source
1. .25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

BASE COUNT
5 a 5 c 8 g 7 t

ORIGIN

Query Match
Best Local Similarity 85.7%; Score 12; DB 6; Length 25;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY
1 CAAGTCCAGNCC 13
20 CAAGTCCAGACC 8

Db

RESULT 3
AR006801 17 bp DNA Linear PAT 04-DEC-1998
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sequence 51 from patent US 5750105.
AR006801
AR006801.1 GI:3966285
Unknown.
Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS
Newman, R.A., Hanna, N. and Raab, R.W.
TITLE
Recombinant antibodies for human therapy
JOURNAL
Patent: US 5750105-A 51 12-MAY-1998;
Location/Qualifiers

FEATURES
source
1. .17
/organism="unknown"

BASE COUNT
3 a 5 c 6 g 3 t

ORIGIN

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 CAAGTCCAGNCCA 14
17 CCAGTCCAGTCCA 4

Db

RESULT 4
AR008981 17 bp DNA Linear PAT 04-DEC-1998
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sequence 1 from patent US 5756096.
AR008981
AR008981.1 GI:3967786
Unknown.
Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS
Newman, R.A., Hanna, N. and Raab, R.W.
TITLE
Recombinant antibodies for human therapy
JOURNAL
Patent: US 5756096-A 1 26-MAY-1998;
Location/Qualifiers

FEATURES
source
1. .17
/organism="unknown"

BASE COUNT
3 a 5 c 6 g 3 t

ORIGIN

Query Match
Best Local Similarity 81.4%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 CAAGTCCAGNCCA 14
17 CCAGTCCAGTCCA 4

Db

RESULT 5
AR135409 17 bp DNA Linear PAT 16-JUN-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sequence 44 from patent US 6136310.
AR135409
AR135409.1 GI:14476081
Unknown.
Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 17)
AUTHORS
Hanna, N., Newman, R. Anthony, and Reff, M. Elliot.
TITLE
Recombinant anti-CD4 antibodies for human therapy
JOURNAL
Patent: US 6136310-A 44 24-OCT-2000;
Location/Qualifiers

FEATURES
source
1. .17
/organism="unknown"

BASE COUNT
3 a 5 c 6 g 3 t

ORIGIN

Query Match
Best Local Similarity 85.7%; Score 11.4; DB 6; Length 17;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY
1 CAAGTCCAGNCCA 14
17 CCAGTCCAGTCCA 4

Db

RESULT 6
I61180 17 bp DNA Linear PAT 07-OCT-1997
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Sequence 5 from patent US 5658570.
I61180
I61180.1 GI:2479128
Unknown.
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 17)
AUTHORS Newman, R.A., Hanna, N., and Raab, R.W.
TITLE Recombinant antibodies for human therapy
JOURNAL Patent: US 5658570-A 5 19-AUG-1997;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 3 a 5 c 6 g 3 t
ORIGIN
Query Match 81.4%; Score 11.4; DB 6; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
17 CCAGTCCAGTCCA 4
Db
RESULT 7
LOCUS I71313 17 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 51 from patent US 5681722.
ACCESSION I71313
VERSION I71313.1 GI:3007448
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Newman, R.A., Hanna, N., and Raab, R.W.
TITLE Recombinant antibodies for human therapy
JOURNAL Patent: US 5681722-A 51 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 3 a 5 c 6 g 3 t
ORIGIN
Query Match 81.4%; Score 11.4; DB 6; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
17 CCAGTCCAGTCCA 4
Db
RESULT 8
LOCUS I78729 17 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 5 from patent US 5693780.
ACCESSION I78729
VERSION I78729.1 GI:3014883
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Newman, R.A., Hanna, N., and Raab, R.W.
TITLE Recombinant antibodies for human therapy
JOURNAL Patent: US 5693780-A 5 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..17
BASE COUNT 3 a 5 c 6 g 3 t
ORIGIN
Query Match 81.4%; Score 11.4; DB 6; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
17 CCAGTCCAGNCCA 14
Db

Db 17 CCAGTCCAGTCCA 4
RESULT 9
LOCUS AX250348/c 18 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 16 from Patent WO0168682.
ACCESSION AX250348
VERSION AX250348.1 GI:15984115
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reim, S.J., and Turpen, T.H.
TITLE Self antigen vaccines for treating b cell lymphomas and other cancers
JOURNAL Patent: WO 0168682-A 16 20-SEP-2001;
FEATURES Large Scale Biology Corporation (US)
Location/Qualifiers
source 1..18
BASE COUNT 4 a 3 c 8 g 3 t
ORIGIN
Query Match 81.4%; Score 11.4; DB 6; Length 18;
Best Local Similarity 85.7%; Pred. No. 5.8e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
15 CCAGTCCAGTCCA 2
Db
RESULT 10
LOCUS AR103422 22 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 13 from patent US 6087473.
ACCESSION AR103422
VERSION AR103422.1 GI:12815010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Konkin, D.C., Foster, D.C., and Gao, Z.
TITLE Kunitz domain polypeptide and materials and methods for making it
JOURNAL Patent: US 6087473-A 13 11-JUL-2000;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 6 a 7 c 7 g 2 t
ORIGIN
Query Match 81.4%; Score 11.4; DB 6; Length 22;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
5 CAAGTCCAGAGCA 18
Db
RESULT 11
LOCUS AR151630 22 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 13 from patent US 6232098.
ACCESSION AR151630
VERSION AR151630.1 GI:15117680
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Konklin,D.C., Foster,D.C. and Gao,Z.
TITLE Kunitz domain polypeptide and materials and methods for making it
JOURNAL Patent: US 6232098-A 13 15-MAY-2001;
FEATURES Location/Qualifiers
source 1..22
BASE COUNT 6 a 7 c 7 g 2 t
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 22;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14
Db 5 CAAGGTCAGAGCA 18
IIIIIIIIII
II

RESULT 12
AX350160/c AX350160 24 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 19 from Patent WO0202775.
DEFINITION AX350160
ACCESSION AX350160
VERSION AX350160.1 GI:18615834
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Boehm,T. and Dear,N.T.
TITLE Calpain protease 12
JOURNAL Patent: WO 0202775-A 19 10-JAN-2002;
FEATURES BASF AKTENGESSELLSCHAFT (DE)
source 1..24
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Capn5-Primer"

BASE COUNT 3 a 7 c 9 g 5 t
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 24;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14
Db 23 CAAGGCCAGTCCA 10
IIIIIIIIII
IIII

RESULT 13
AR006770/c AR006770 26 bp DNA linear PAT 04-DEC-1998
LOCUS Sequence 20 from patent US 5750105.
DEFINITION AR006770
ACCESSION AR006770
VERSION AR006770.1 GI:3966254
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Newman,R.A., Hanna,N. and Raab,R.W.
TITLE Recombinant antibodies for human therapy
JOURNAL Patent: US 5750105-A 20 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 26;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14
Db 26 CCAGGTCAGTCCA 13
IIIIIIIIII
IIII

RESULT 14
AR135378/c AR135378 26 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 13 from patent US 6136310.
DEFINITION AR135378
ACCESSION AR135378
VERSION AR135378.1 GI:14476050
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Hanna,N., Newman,R.Anthony. and Refl,M.Elliott.
TITLE Recombinant anti-CD4 antibodies for human therapy
JOURNAL Patent: US 6136310-A 13 24-OCT-2000;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 26;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14
Db 26 CCAGGTCAGTCCA 13
IIIIIIIIII
IIII

RESULT 15
I71282/c I71282 26 bp DNA linear PAT 03-APR-1998
LOCUS Sequence 20 from patent US 5681722.
DEFINITION I71282
ACCESSION I71282
VERSION I71282.1 GI:3007417
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Newman,R.A., Hanna,N. and Raab,R.W.
TITLE Recombinant antibodies for human therapy
JOURNAL Patent: US 5681722-A 20 28-OCT-1997;
FEATURES Location/Qualifiers
source 1..26
/organism="unknown"

BASE COUNT 7 a 6 c 8 g 5 t
ORIGIN

Query Match 81.4%; Score 11.4; DB 6; Length 26;
Best Local Similarity 85.7%; Pred. No. 5.7e+04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCAGNCCA 14
Db 26 CCAGGTCAGTCCA 13
IIIIIIIIII
IIII

Search completed: June 21, 2003, 22:14:42
Job time : 284.094 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 76.7812 Seconds
(without alignments)
410.621 Million cell updates/sec

Title: US-09-964-666-14

Perfect score: 14
Sequence: 1 CAAGGTCCAGNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	85.7	24	AB000274	Oligonucleotide ad
C 2	12	85.7	24	AB004512	Oligonucleotide ad
C 3	12	85.7	24	AB004553	Oligonucleotide ad
C 4	12	85.7	24	AB010840	Oligonucleotide ad
C 5	12	85.7	24	AB010881	Oligonucleotide ad
C 6	12	85.7	25	AB012376	Oligonucleotide ad
C 7	12	85.7	25	AB012417	Oligonucleotide ad
C 8	11.4	81.4	17	AA035925	Human/monkey heavy
C 9	11.4	81.4	18	AA095155	Human or monkey Ig

C 10	11.4	81.4	17	AA091566	Cynomolgus monkey
C 11	11.4	81.4	17	AA062902	VH1 heavy chain va
C 12	11.4	81.4	17	AA031430	Cynomolgus immunog
C 13	11.4	81.4	17	AA023793	Primer for Anti-CD
C 14	11.4	81.4	17	AA050563	Human/monkey heavy
C 15	11.4	81.4	18	AA043427	VH1 Family Specific
C 16	11.4	81.4	18	AA045544	Tumour-specific Ig
C 17	11.4	81.4	18	AA024764	5' PCR primer used
C 18	11.4	81.4	20	AA064442	Mouse ada gene rep
C 19	11.4	81.4	20	AA012663	Human BAX RT-PCR p
C 20	11.4	81.4	20	AA099913	Primer used to amp
C 21	11.4	81.4	22	AA050117	Human serine prote
C 22	11.4	81.4	22	AA046336	Human zkus5 kunitz
C 23	11.4	81.4	22	AA014335	Human lymphoma-spe
C 24	11.4	81.4	22	AA055000	Human lymphoma-spe
C 25	11.4	81.4	24	AA099782	Murine capn5 Set 1
C 26	11.4	81.4	25	AA075424	Primer for human a
C 27	11.4	81.4	26	AA035905	Human/monkey heavy
C 28	11.4	81.4	26	AA095124	Human or monkey Ig
C 29	11.4	81.4	26	AA092201	Monkey/human heavy
C 30	11.4	81.4	26	AA062871	Human or monkey VH
C 31	11.4	81.4	26	AA031384	Human or monkey he
C 32	11.4	81.4	26	AA023762	Primer for Anti-CD
C 33	11.4	81.4	26	AA005652	Human/monkey, Vh1 e
C 34	11.4	81.4	27	AA087238	Primer for leader
C 35	11.4	81.4	27	AA092804	Primer H51 for hum
C 36	11.4	81.4	27	AA052801	PCR primer H51 fro
C 37	11.4	81.4	27	AA009964	Primer H51 for hum
C 38	11.4	81.4	29	AA047905	IgE antibody L cha
C 39	11.4	81.4	30	AA067195	Humanized 130BF VH
C 40	11.4	81.4	30	AA056586	Heavy chain primer
C 41	11.4	81.4	30	AA016179	Humanised antibody
C 42	11.4	81.4	30	AA033320	Anti-CD23 6G5 anti
C 43	11.4	81.4	32	AA018053	Sense primer #1 am
C 44	11.4	81.4	34	AA061365	Human Immunoglobul
C 45	11.4	81.4	34	AA078273	Human Ig H chain s

ALIGNMENTS

RESULT 1	AB000274/c	
ID	AB000274 standard; DNA: 24 BP.	
AC	AB000274:	
XX		
XX	11-JUN-2002 (first entry)	
DT		
DT	Oligonucleotide adapter/capture probe 265.	
DE		
XX	Oligonucleotide array; adapter sequence; probe; ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200216649-A2.	
XX		
PD	28-FEB-2002.	
XX		
XX	27-AUG-2001: 2001WO-0526519.	
PF		
XX	25-AUG-2000: 2000US-227948P.	
PR	29-AUG-2000: 2000US-228854P.	
XX		
PA	(ILLU-) ILLUMINA INC.	
XX		
XX	Gunderson K:	
PI		
XX		
DR	WPI: 2002-292068/33.	
XX		
PT	Array comprising adapter sequences useful for immobilizing or detecting	
PT	a target nucleic acid sequence, has different addresses comprising	
PT	different specific capture probes	

XX Claim 1; Page 50; 261pp; English.
PS
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
SO Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
XX
XX
Query Match 85.7%; Score 12; DB 24; Length 24;
Best Local Similarity 92.3%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CAAGGTCAGNCC 13
11-JUN-2002 (first entry)
DB 19 CAAGGTCAGACC 7
XX
XX
RESULT 2
ABQ04512/c
ID ABQ04512 standard; DNA; 24 BP.
XX
XX ABQ04512;
XX
XX 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 4503.
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
XX
XX Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US26519.
XX
XX 25-AUG-2000; 2000US-227948P.
XX
XX 29-AUG-2000; 2000US-228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting
XX a target nucleic acid sequence, has different addresses comprising
XX different specific capture probes
XX
XX Claim 1; Page 145; 261pp; English.
XX
XX
PS The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
XX nucleic acid sequence by attaching a adapter nucleic acid
XX (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
XX nucleic acid and contacting the modified target nucleic acid with (I).
XX The steps of above method is useful for detecting a target nucleic acid,
XX which further comprises detecting the presence of the modified target
XX nucleic acid.
XX
XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
XX
XX
DT Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;

XX Query Match 85.7%; Score 12; DB 24; Length 24;
PS Best Local Similarity 92.3%; Pred. No. 2.1e+03;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CAAGGTCAGNCC 13
11-JUN-2002 (first entry)
DB 19 CAAGGTCAGACC 7
XX
XX
RESULT 3
ABQ04553
ID ABQ04553 standard; DNA; 24 BP.
XX
XX ABQ04553;
XX
XX 11-JUN-2002 (first entry)
XX
XX Oligonucleotide adapter/capture probe 4544.
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
XX
XX Synthetic.
XX
XX WO200216649-A2.
XX
XX 28-FEB-2002.
XX
XX 27-AUG-2001; 2001WO-US26519.
XX
XX 25-AUG-2000; 2000US-227948P.
XX
XX 29-AUG-2000; 2000US-228854P.
XX
XX (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
XX
XX WPI; 2002-292068/33.
XX
XX Array comprising adapter sequences useful for immobilizing or detecting
XX a target nucleic acid sequence, has different addresses comprising
XX different specific capture probes
XX
XX Claim 1; Page 145; 261pp; English.
XX
XX
CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
CC
CC Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 other;
CC
CC
OY 1 CAAGGTCAGNCC 13
11-JUN-2002 (first entry)
DB 6 CAAGGTCAGACC 18
XX
XX
RESULT 4
ABQ10840/c
ID ABQ10840 standard; DNA; 24 BP.
XX
XX ABQ10840;
XX
XX 11-JUN-2002 (first entry)
XX
XX
DT 11-JUN-2002 (first entry)

XX Oligonucleotide adapter/capture probe 10831.
DE Oligonucleotide array; adapter sequence; probe; ss.
XX Synthetic.
OS
XX WO200216649-A2.
PN
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US26519.
PF
XX 25-AUG-2000; 2000US-227948P.
PR
XX 29-AUG-2000; 2000US-228854P.
PR
XX (ILLU-) ILLUMINA INC.
PA
XX Gunderson K;
PI
XX WPI; 2002-292068/33.
DR
XX
XX Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes
PS Claim 1; Page 223; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
CC
XX Sequence 24 BP; 5 A; 5 C; 8 G; 6 T; 0 other;
SQ
Query Match 85.7%; Score 12; DB 24; Length 24;
Best Local Similarity 92.3%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCCAGACC 13
DB 19 CAAGTCCAGACC 7
RESULT 5
ABQ10881
ID ABQ10881 standard; DNA; 24 BP.
XX
XX ABQ10881;
AC
XX
XX 11-JUN-2002 (first entry)
DT
XX Oligonucleotide adapter/capture probe 10872.
DE
XX Oligonucleotide array; adapter sequence; probe; ss.
KM
XX Synthetic.
OS
XX WO200216649-A2.
PN
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US26519.
PF
XX 25-AUG-2000; 2000US-227948P.
PR
XX 29-AUG-2000; 2000US-228854P.
PR
XX

PA (ILLU-) ILLUMINA INC.
XX
XX Gunderson K;
PI
XX WPI; 2002-292068/33.
DR
XX
XX Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes
PS Claim 1; Page 223; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (I).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.
CC
XX Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 other;
SQ
Query Match 85.7%; Score 12; DB 24; Length 24;
Best Local Similarity 92.3%; Pred. No. 2.1e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CAAGTCCAGACC 13
DB 6 CAAGTCCAGACC 18
RESULT 6
ABQ12376/C
ID ABQ12376 standard; DNA; 25 BP.
XX
XX ABQ12376;
AC
XX
XX 11-JUN-2002 (first entry)
DT
XX Oligonucleotide adapter/capture probe 12367.
DE
XX Oligonucleotide array; adapter sequence; probe; ss.
KM
XX Synthetic.
OS
XX WO200216649-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 27-AUG-2001; 2001WO-US26519.
PF
XX 25-AUG-2000; 2000US-227948P.
PR
XX 29-AUG-2000; 2000US-228854P.
PR
XX (ILLU-) ILLUMINA INC.
PA
XX Gunderson K;
PI
XX WPI; 2002-292068/33.
DR
XX
XX Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes
PS Claim 1; Page 242; 261pp; English.
XX
XX The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in ABQ00010-ABQ13409. (I) is useful for immobilising a target

CC nucleic acid sequence by attaching a adapter nucleic acid
CC (AB000010-AB013409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (1).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.

XX Sequence 25 BP: 5 A; 5 C; 8 G; 7 T; 0 other;

Query Match 85.7%; Score 12; DB 24; Length 25;

Best Local Similarity 92.3%; Pred. No. 2.1e+03; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCC 13
DB 20 CAAGGTCAGACC 8

RESULT 7

AB012417 standard; DNA: 25 BP.

XX AB012417;

XX 11-JUN-2002 (first entry);

DE Oligonucleotide adapter/capture probe 12408.

XX Oligonucleotide array; adapter sequence; probe; ss.

OS Synthetic.

XX WO200216649-A2.

XX 28-FEB-2002.

XX 27-AUG-2001; 2001WO-US26519.

XX 25-AUG-2000; 2000US-227948P.

XX 29-AUG-2000; 2000US-228854P.

PA (ILLU-) ILLUMINA INC.

XX Gunderson K;

XX WPI; 2002-292068/33.

PT Array comprising adapter sequences useful for immobilizing or detecting
PT a target nucleic acid sequence, has different addresses comprising
PT different specific capture probes

PS Claim 1; Page 242; 261pp; English.

CC The invention relates to an oligonucleotide array (I) comprising at least
CC 25 different addresses (adapter sequences) with each comprising a
CC different capture probe selected from a group consisting of the sequences
CC given in AB000010-AB013409. (I) is useful for immobilizing a target
CC nucleic acid sequence by attaching a adapter nucleic acid
CC (AB000010-AB013409) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with (1).
CC The steps of above method is useful for detecting a target nucleic acid,
CC which further comprises detecting the presence of the modified target
CC nucleic acid.

XX Sequence 25 BP: 6 A; 8 C; 5 G; 6 T; 0 other;

Query Match

Best Local Similarity 85.7%; Score 12; DB 24; Length 25;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCC 13

DB 7 CAAGGTCAGACC 19

RESULT 8

AA035925/C

ID AA035925 standard; DNA: 17 BP.

XX AA035925;

DE 08-JUN-1993 (first entry)

XX Human/monkey heavy chain variable region primer VH1.

XX Amplify: polymerase chain reaction; heavy: light; chain: variable; Ig;

XX PCR: primer: region; lambda: human; constant: antigen; recombinant;

XX antibody; chimpanzee; Ag; old world monkey; eczema; immunoglobulin;

XX therapeutic; rheumatoid arthritis; P-Bluescript; ss.

XX Synthetic.

XX WO9302108-A.

XX 04-FEB-1993.

XX 24-JUL-1992; 92WO-US06194.

XX 25-JUL-1991; 91US-0735064.

XX 23-MAR-1992; 92US-0856281.

PA (IDEC-) IDEC PHARM CORP.

XX Hanna N, Newman RA, Raab RW;

XX WPI; 1993-058729/07.

CC The sequences given in AA035925-30 represent sense primers which were
CC used to amplify cynomolgus heavy chain variable region sequences.
CC The amplified sequences belonged to a number of different gene
CC families. The amplified sequences were cloned into p-Bluescript
CC for sequencing. The amplified sequences could be used in the
CC production of a recombinant antibody, comprising a human, chimpanzee
CC or old world monkey immunoglobulin (Ig) constant region and an antigen
CC (Ag) binding portion of an old world monkey Ig variable region, where
CC the old world monkeys may be the same or different. The recombinant
CC antibody may be used as a therapeutic agent for the treatment of
CC rheumatoid arthritis, eczema and immunological disorders.

XX Sequence 17 BP: 3 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 14; Length 17;

Best Local Similarity 85.7%; Pred. No. 4.6e+03; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCAGNCCA 14

DB 17 CCAGTCAGTCCA 4

RESULT 9

AA095155/C

ID AA095155 standard; DNA: 17 BP.

XX AA095155;

XX 18-FEB-1998 (first entry)

XX Human or monkey Ig heavy chain variable region primer VH1.

XX Old World monkey; immunoglobulin; Ig; heavy chain; CD4;
 KW human; variable region; chimeric antibody;
 KW B cell lymphoma; infectious disease; AIDS; autoimmune disease;
 KW inflammatory disease; transplant rejection; imaging reagent;
 KW vaccine; immunogen; immunotherapy; anti-idiotypic response;
 KW immunosuppression; treatment; prevention; proliferative disease;
 KW hyperproliferative disease; immunologically mediated disease;
 KW rheumatoid arthritis; lupus erythematosus; PCR primer;
 KW systemic lupus erythematosus; SLE; Hashimoto's thyroiditis;
 KW multiple sclerosis; myasthenia gravis; type 1 diabetes; uveitis;
 KW neoplastic syndrome; psoriasis; atopic dermatitis;
 KW contact dermatitis; eczematous dermatitis; seborrheic dermatitis;
 KW lichen planus; pemphigus; bullous pemphigus; Epidermolysis bullosa;
 KW urticaria; angioedema; vasculitis; erythema;
 KW cutaneous eosinophilia; alopecia areata;
 KW reversible obstructive airways disease; intestinal inflammation;
 KW intestinal allergy; Coeliac disease; proctitis; eosinophilia;
 KW gastroenteritis; mastocytosis; Crohn's disease; ulcerative colitis;
 KW food related allergy; migraine; rhinitis; eczema;
 KW non-immunogenic; ss.
 XX Synthetic;
 OS Homo sapiens.
 OS Cebus apella.
 XX US5681722-A.
 PN 28-OCT-1997.
 PD 07-JUN-1995; 95US-0478039.
 XX 10-JUL-1992; 92US-0912292.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 25-JAN-1995; 95US-0379072.
 PR 07-JUN-1995; 95US-0478039.
 XX (IDEC-) IDEC PHARM CORP.
 PA Hanna N, Newman RA, Raab RW.
 PI WPI: 1997-535052/49.
 DR Production of humanised antibodies containing monkey variable region
 PT - used for the treatment of B cell lymphoma, autoimmune disease,
 PT inflammatory disease and infection, e.g. by HIV
 XX Example 1; Fig 8; 84pp; English.
 PS The present sequence is a PCR primer for a human or monkey
 XX immunoglobulin heavy chain variable region cDNA, which
 CC was used in the development of a novel method for producing a
 CC chimeric antibody (Ab), comprising the variable region of an Old
 CC World monkey (OMW) Ab and the constant region of a human Ab. The
 CC method comprises amplifying DNA from the OMW using a primer
 CC complementary to the 5' leader sequence of the OMW Ab gene and
 CC fusing the resulting variable region coding sequence with a human
 CC constant region coding sequence.
 CC The chimeric Ab may be used as a passive or active therapeutic for
 CC B cell lymphoma, infectious, e.g. AIDS, autoimmune and inflammatory
 CC diseases and transplant rejection. The Ab can be used in its native
 CC form or as part of an Ab/chelate, Ab/drug or Ab/toxin complex.
 CC Additionally, a whole Ab, or a fragment (Fab2, Fab, Fv) may be used
 CC as an imaging reagent or as a potential vaccine or immunogen in
 CC active immunotherapy to generate anti-idiotypic responses.
 CC An anti-CD4 recombinant Ab, or a fragment can also be used to
 CC induce immunosuppression and can therefore be used to treat or
 CC prevent resistance to, or rejection of transplanted organs or
 CC tissues, autoimmune, inflammatory, proliferative and
 CC hyperproliferative diseases, cutaneous manifestations of
 CC immunologically mediated diseases (e.g. rheumatoid arthritis, lupus
 CC erythematosus, systemic lupus erythematosus, Hashimoto's

CC thyroiditis, multiple sclerosis, myasthenia gravis, type 1
 CC diabetes, uveitis, neoplastic syndrome, psoriasis, atopic
 CC dermatitis, contact dermatitis and further eczematous dermatitis;
 CC seborrheic dermatitis, lichen planus, pemphigus, bullous pemphigus,
 CC epidermolysis bullosa, urticaria, angioedema, vasculitis,
 CC erythema, cutaneous eosinophilias, alopecia areata), reversible
 CC obstructive airways disease, intestinal inflammations and
 CC allergies (e.g. Coeliac disease, proctitis, eosinophilia
 CC gastroenteritis, mastocytosis, Crohn's disease and ulcerative
 CC colitis) and food related allergies (e.g. migraine, rhinitis and
 CC eczema).
 CC The Ab of the invention is non-immunogenic and therefore does not
 CC induce a human anti-Ab response. It also has a relatively long
 CC half-life and a full effector function with human cells and
 CC complement.
 XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other;
 SO Query Match 81.4%; Score 11.4; DB 18; Length 17;
 Best Local Similarity 85.7%; Pred. No. 4.6e+03;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CAAGTCCAGNCA 14
 Db 17 CCAGTCCAGTCCA 4
 RESULT 10
 AAT91566/c
 ID AAT91566 standard; DNA: 17 BP.
 XX AAT91566;
 AC 16-JAN-1998 (first entry)
 XX Cynomolgus monkey heavy chain variable region primer VH1.
 DE Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
 KW antigen binding region; tumour; PCR; polymerase chain reaction; ss.
 XX Synthetic.
 OS US5658570-A.
 PN 19-AUG-1997.
 PD 25-JUL-1991; 91US-0735064.
 PR 10-JUL-1992; 92US-0912292.
 PR 25-JUL-1991; 91US-0735064.
 PR 23-MAR-1992; 92US-0856281.
 PR 25-JAN-1995; 95US-0379072.
 XX (IDEC-) IDEC PHARM CORP.
 PA Hanna N, Newman RA, Raab RW.
 PI WPI: 1997-424183/39.
 DR Chimeric antibodies for human therapy - comprising human or
 PT chimpanzee immunoglobulin constant region and an Old World monkey
 PT antigen-binding region
 XX Example 1; Fig 8; 46pp; English.
 PS A new chimeric antibody (Ab) has been developed comprising a human or
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
 CC antigen (Ag)-binding region. An anti-CD4 antibody (Ab) comprising the
 CC light- and heavy-chain variable regions encoded by AAT91564 and AAT91565
 CC is also new. The present sequence represents a primer, VH1, used in the
 CC amplification of cynomolgus monkey immunoglobulin heavy chain regions.
 CC The Abs are useful for human therapy, especially of tumours. Old world


```

OS Synthetic:
XX Primate sp:
XX
XX US5750105-A.
XX
XX 12-MAY-1998.
XX
XX 07-JUN-1995; 95US-0476349.
XX
XX 10-JUL-1992; 92US-0912292.
PR 25-JUL-1991; 91US-0735064.
PR 23-MAR-1992; 92US-0856281.
PR 05-DEC-1995; 95US-0379072.
PR 07-JUN-1995; 95US-0476349.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Raab RW;
XX
XX WPI: 1998-296690/26.
XX
XX Improved method for antibody treatment - uses an antibody comprising
XX an Old World monkey variable region and a human constant domain
XX
XX Example 1: Fig 8; 84pp; English.
XX
XX This sequence is a PCR primer for DNA encoding an anti-CD4 antibody
XX (Ab). The amplified sequence can be used in the method of the invention
XX for treating a subject, where the treatment comprises administration of
XX an Ab. The method comprises the administration of an antibody which has
XX an Old World monkey (e.g. baboon or macaque) variable region which binds
XX to an antigen (Ag) (or Ag binding portion), and a human constant domain.
XX The method is useful for the treatment of eczema and immuno-modulated
XX diseases and especially rheumatoid arthritis. The recombinant antibodies
XX used are sufficiently different from native monkey antibodies to allow
XX human antigens to raise these antibodies, but similar enough to human
XX antibody so there is no immune response to the antibodies in humans.
XX Compared to antibodies used in therapy in prior art, these antibodies do
XX not induce human anti-antibodies on repeated administration. They also
XX have longer half-lives and do not have a lack of effector function with
XX human cells.
XX
XX Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other:
XX
XX Query Match 81.4%; Score 11.4; DB 19; Length 17;
XX Best Local Similarity 85.7%; Pred. No. 4.6e+03;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX
OY 1 CAAGGTCACAGNCA 14
XX | | | | | | | | | |
XX Db 17 CCAGGTCACAGTCA 4
XX
XX RESULT 14
XX AAV05683/C
XX ID AAV05683 standard; DNA: 17 BP.
XX
XX AAV05683;
XX
XX 05-MAY-1998 (first entry)
XX
XX Human/monkey heavy chain variable region primer VH1.
XX
XX Primer: PCR: amplification; leader sequence: human; monkey; baboon;
XX macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
XX lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
XX tumour; antibody; ss.
XX
XX Synthetic:
XX OS Homo sapiens.
XX OS Macaca sp.
XX OS Papio sp.
XX

```

PN	US5693780-A.
XX	
XD	02-DEC-1997.
XX	
PF	07-JUN-1995; 95US-0481869.
XX	
PR	10-JUL-1992; 92US-0912292.
ER	25-JUL-1991; 91US-0735064.
PR	23-MAR-1992; 92US-0856281.
PR	25-JAN-1995; 92US-0379072.
PR	07-JUN-1995; 95US-0481869.
PA	(IDEC-) IDEC PHARM CORP.
P1	Hanna N, Newman RA, Raab RW;
DR	WPI; 1998-031820/03.
XX	
PT	Nucleic acid encoding hybrid antibody - comprising monkey
PT	antigen-binding region and human or chimp constant region
XX	
PS	Example 1; Fig 8; 46pp; English.
CC	
CC	This sequence represents a sense primer derived by comparing sequences
CC	from human and monkey (especially baboon (Papio sp.) and macaque
CC	(Macaca sp.) immunoglobulin (Ig) heavy chain regions. The primer is
CC	used to amplify the monkey heavy chain variable region for construction
CC	of a recombinant antibody comprising: (i) an Old World monkey Ig
CC	antigen-binding region; and (ii) a human or chimpanzee Ig constant
CC	region. The hybrid antibodies can be used as passive or active
CC	therapeutic agents against human diseases, e.g. B-cell lymphoma, AIDS,
CC	autoimmune and inflammatory diseases, transplant rejection or tumours,
CC	or for producing therapeutic and diagnostic conjugates. Although
CC	evolutionary distant monkeys are used to raise antibodies against human
CC	antigens, they are sufficiently similar that they produce antibodies
CC	similar to human antibodies, such when the monkey antibodies are
CC	introduced into humans, no host anti-antibody response is stimulated.
XX	
XQ	Sequence 17 BP; 3 A; 5 C; 6 G; 3 T; 0 other:
QY	
DB	Query Match 81.4%; Score 11.4; DB 19; Length 17; Best Local Similarity 85.7%; Pred. No. 4.6e+03; Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps
QY	1 CAAGGTCACAGNCA 14 17 CCAGGTCCAGTCCA 4
DB	
RESULT 15	
ID	AAT43427/C
XX	AAT43427 standard; DNA: 18 BP.
NC	AAT43427;
XX	
DT	17-FEB-1997 (first entry)
DE	VH1 family specific primer for human heavy chain Ig.
XX	
KV	Xenograft rejection; xenotransplantation; organ transplant;
KW	animal model; p1g; monoclonal antibody; primer; PCR;
KW	polymerase chain reaction; phage display; ss.
OS	Synthetic.
PN	WO9636358-A1.
PD	21-NOV-1996.
PF	14-MAY-1996; 96WO-US06804.
PR	15-MAY-1995; 95US-0440621.
XX	

PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX
 PI Cramer DV, Makowka L, Wu G;
 XX
 DR WPI: 1997-011852/01.
 XX

PT Inhibiting xenograft rejection by modifying antigen expression of
 PT the graft - prevents binding of anti-donor antibody and prolongs
 PT graft survival
 XX

PS Example 16; Page 121; 135pp; English.
 XX

CC PCR primers VH1-VH6 (AAT43427-32) are Ig family specific heavy chain
 CC 5' primers designed for the amplification of antibody VH region
 CC cDNA and for the introduction of cohesive termini compatible with
 CC directional ligation into the unique NotI or SpeI sites of the
 CC SurZAP vector. They were used with 3' primers in the PCR
 CC amplification of antibody heavy chain variable region cDNA from
 CC lymphocytes of a human transplant patient who had received a
 CC porcine xenograft. A human IgM heavy chain, human Igk light
 CC chain Fab library was generated using phage display and panned for
 CC anti-donor xenograft antibody sequences.
 XX

SO Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 other;

Query Match 81.4%; Score 11.4; DB 18; Length 18;
 Best Local Similarity 85.7%; Pred. No. 4.6e+03;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGGTCCAGNCCA 14
 I | | | | | | | | | |
 DB 17 CCAGGTCCAGTCCA 4

Search completed: June 21, 2003, 22:26:29
 Job time : 78.7812 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 16.625 Seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-14
Perfect score: 14
Sequence: 1 CAAGCTCCAGNCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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2: /cgn2_6/pdata/1/lna/5B.COMB.seq:*
3: /cgn2_6/pdata/1/lna/6A.COMB.seq:*
4: /cgn2_6/pdata/1/lna/6B.COMB.seq:*
5: /cgn2_6/pdata/1/lna/PCrUS.COMB.seq:*
6: /cgn2_6/pdata/1/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
C 1	11.4	81.4	17	US-08-379-072A-5	Sequence 5, Appl
C 2	11.4	81.4	17	US-08-478-039-51	Sequence 51, Appl
C 3	11.4	81.4	17	US-08-481-869-5	Sequence 5, Appl
C 4	11.4	81.4	17	US-08-476-349A-51	Sequence 51, Appl
C 5	11.4	81.4	17	US-08-523-894-44	Sequence 1, Appl
C 6	11.4	81.4	17	US-09-320-095-13	Sequence 44, Appl
C 7	11.4	81.4	22	US-09-523-487-13	Sequence 13, Appl
C 8	11.4	81.4	22	US-08-478-039-20	Sequence 13, Appl
C 9	11.4	81.4	26	US-08-476-349A-20	Sequence 20, Appl
C 10	11.4	81.4	26	US-08-523-894-13	Sequence 13, Appl
C 11	11.4	81.4	27	US-08-646-367-3	Sequence 3, Appl
C 12	11.4	81.4	30	US-08-373-190-59	Sequence 59, Appl
C 13	11.4	81.4	30	US-08-438-190A-59	Sequence 59, Appl
C 14	11.4	81.4	30	US-08-803-085-14	Sequence 14, Appl
C 15	11.4	81.4	30	US-09-287-145A-59	Sequence 59, Appl
C 16	11.4	81.4	30	US-09-556-111-59	Sequence 59, Appl
C 17	11.4	81.4	34	US-08-814-412-21	Sequence 21, Appl
C 18	11.4	81.4	35	PCT-US94-14106-23	Sequence 23, Appl
C 19	11.4	81.4	38	US-08-026-320A-5	Sequence 5, Appl
C 20	11.4	81.4	38	US-08-761-277A-52	Sequence 52, Appl
C 21	11.4	81.4	46	US-07-916-098A-60	Sequence 60, Appl
C 22	10.4	81.4	23	US-09-081-646-339	Sequence 339, App
C 23	10.4	74.3	15	US-09-184-658-24	Sequence 24, Appl
C 24	10.4	74.3	20	US-09-184-658-25	Sequence 25, Appl
C 25	10.4	74.3	20	US-09-289-267-64	Sequence 64, Appl
C 26	10.4	74.3	20	US-08-437-607A-28	Sequence 28, Appl
C 27	10.4	74.3	2		

C 28	10.4	74.3	21	4	US-08-949-155-16	Sequence 16, Appl
C 29	10.4	74.3	21	4	US-09-819-964-16	Sequence 16, Appl
C 30	10.4	74.3	22	4	US-09-487-792-50	Sequence 50, Appl
C 31	10.4	74.3	24	2	US-08-691-814B-53	Sequence 53, Appl
C 32	10.4	74.3	25	4	US-09-462-136-10	Sequence 10, Appl
C 33	10.4	74.3	26	2	US-08-859-998-653	Sequence 653, App
C 34	10.4	74.3	26	4	US-09-225-928-653	Sequence 653, App
C 35	10.4	74.3	28	5	PCT-US94-10957-19	Sequence 19, Appl
C 36	10.4	74.3	30	2	US-08-924-440-4	Sequence 4, Appl
C 37	10.4	74.3	39	6	5187077-19	Patent No. 5187077
C 38	10.4	74.3	39	6	5427925-17	Patent No. 5427925
C 39	10.4	74.3	43	3	US-08-589-939-61	Sequence 61, Appl
C 40	10	71.4	20	1	US-07-767-135-17	Sequence 17, Appl
C 41	10	71.4	20	1	US-07-841-652-8	Sequence 8, Appl
C 42	10	71.4	20	3	US-09-289-267-65	Sequence 65, Appl
C 43	10	71.4	20	4	US-09-746-694-40	Sequence 40, Appl
C 44	10	71.4	22	1	US-08-379-081B-314	Sequence 314, App
C 45	10	71.4	22	1	US-08-379-078-314	Sequence 314, App

ALIGNMENTS

RESULT 1
; Sequence 5, Application US/08379072A
; Patent No. 5658570
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: HANNA, Nabil
; APPLICANT: RAAB, Ronald W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379, 072A
; FILING DATE: 25-JAN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 012712-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-379-072A-5

Query Match 81.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14
17 CCAGGTCAGTCCA 4

RESULT 2

US-08-478-039-51/c
; Sequence 51, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: NO
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: heavy chain variable region
; US-08-478-039-51

Query Match 81.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14
17 CCAGGTCAGTCCA 4

Db 17 CCAGGTCAGTCCA 4

RESULT 3

US-08-481-869-5/c
; Sequence 5, Application US/08481869
; Patent No. 5693780
; GENERAL INFORMATION:
; APPLICANT: NEWMAN, Roland A.
; APPLICANT: HANNA, Nabil W.
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,869
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,072A
; FILING DATE: 25-JAN-1995
; APPLICATION NUMBER: US/07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 012712-067
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-481-869-5

Query Match 81.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14
17 CCAGGTCAGTCCA 4

RESULT 4

US-08-476-349A-51/c
; Sequence 51, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil W.
; APPLICANT: Raab, Ronald W.

TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: NO
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain variable region
US-08-476-349A-51
Query Match 81.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
1 | | | | | | | | | |
Db 17 CCAGTCCAGTCCA 4
RESULT 5
US-08-476-237-1/C
Sequence 1, Application US/08476237
Patent No. 5756096
GENERAL INFORMATION:
APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia

COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,237
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-237-1
Query Match 81.4%; Score 11.4; DB 1; Length 17;
Best Local Similarity 85.7%; Pred. No. 5.8e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CAAGTCCAGNCCA 14
1 | | | | | | | | | |
Db 17 CCAGTCCAGTCCA 4
RESULT 6
US-08-523-894-44/C
Sequence 44, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 17 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VHL heavy chain variable region
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; US-08-523-894-44
;
Query Match
Best Local Similarity 81.4%; Score 11.4; DB 3; Length 17;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
Db 17 CCAGTCCAGTCCA 4

RESULT 7
US-09-320-095-13
; Sequence 13, Application US/09320095
; Patent No. 6087473
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/320,095
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: US 60/087,032
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC15,999
;
; US-09-320-095-13
;
Query Match
Best Local Similarity 81.4%; Score 11.4; DB 3; Length 22;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
Db 5 CAAGTCCAGAGCA 18

RESULT 8
US-09-523-487-13
; Sequence 13, Application US/09523487
; Patent No. 6232098
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/523,487
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26

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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer ZC15,999
;
; US-09-523-487-13
;
Query Match
Best Local Similarity 81.4%; Score 11.4; DB 4; Length 22;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
Db 5 CAAGTCCAGAGCA 18

RESULT 9
US-08-478-039-20/c
; Sequence 20, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

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ORGANISM: Homo sapiens or Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain primers with SalI site
US-08-478-039-20

Query Match 81.4%; Score 11.4; DB 1; Length 26;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
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Db 26 CCAGTCCAGTCCA 13

RESULT 10
US-08-476-349A-20/C
Sequence 20, Application US/08476349A
Patent No. 5750105
GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabli
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince St.
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens or Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: heavy chain primers with SalI site
US-08-476-349A-20

Query Match 81.4%; Score 11.4; DB 1; Length 26;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
| | | | | | | | | | | | | | | | | |
Db 26 CCAGTCCAGTCCA 13

RESULT 11
US-08-523-894-13/C
Sequence 13, Application US/08523894
Patent No. 6136310
GENERAL INFORMATION:
APPLICANT: Hanna, Nabli
APPLICANT: Newman, Roland A.
APPLICANT: Reif, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human or Monkey
POSITION IN GENOME:
CHROMOSOME/SEGMENT: VH1 leader sequence
US-08-523-894-13

Query Match 81.4%; Score 11.4; DB 3; Length 26;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCCAGNCCA 14
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Db 26 CCAGTCCAGTCCA 13

RESULT 12
US-08-646-367-3/C
Sequence 3, Application US/08646367
Patent No. 5959085
GENERAL INFORMATION:
APPLICANT: Pierre Garrone
APPLICANT: Odile Djossou

```

? APPLICANT: Francois Fossiez
? APPLICANT: Jacques Bancheureau
? TITLE OF INVENTION: Human Monoclonal Antibodies
? TITLE OF INVENTION: Against Human Cytokines And
? TITLE OF INVENTION: Methods Of Making And Using Such Antibodies
? NUMBER OF SEQUENCES: 30
? CORRESPONDENCE ADDRESS:
? ADDRESS: Schering-Plough Corporation
? STREET: 2000 Gallopings Hill Road
? CITY: Kenilworth
? STATE: New Jersey
? COUNTRY: USA
? ZIP: 07033
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: Apple Macintosh
? OPERATING SYSTEM: Macintosh 7.5.3
? SOFTWARE: Microsoft Word 5.1a
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/646,367
? FILING DATE: May 16, 1996
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Foulke, Cynthia L.
? REGISTRATION NUMBER: 32,364
? REFERENCE/DOCKET NUMBER: SF0403K
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 908-298-2987
? TELEFAX: 908-298-5388
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 27 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
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? US-08-646-367-3
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Query Match      81.4%; Score 11.4; DB 2; Length 27;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      1 CAAGGTCACAGNCCA 14
DB      24 CCAGGTCACAGTCCA 11
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RESULT 13
US-08-373-190-59/C
? Sequence 59, Application US/08373190
? Patent No. 5851829
? GENERAL INFORMATION:
? APPLICANT: MARASCO, WAYNE
? APPLICANT: HASSETLINE, WILLIAM
? TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
? NUMBER OF SEQUENCES: 79
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
? STREET: 130 WATER STREET
? CITY: BOSTON
? STATE: MA
? COUNTRY: US
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/373,190
? FILING DATE: 17-JAN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US93/06735

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? FILING DATE: 16-JUL-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: RESNICK, DAVID S
? REGISTRATION NUMBER: 34,235
? REFERENCE/DOCKET NUMBER: 41956-PCT-US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-523-3400
? TELEFAX: 617-523-6440
? TELEX: STRE UR 2002
? INFORMATION FOR SEQ ID NO: 59:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 30 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
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? US-08-373-190-59
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Query Match      81.4%; Score 11.4; DB 2; Length 30;
Best Local Similarity 85.7%; Pred. No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB      27 CCAGGTCACAGTCCA 14
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RESULT 14
US-08-438-190A-59/C
? Sequence 59, Application US/08438190A
? Patent No. 5965371
? GENERAL INFORMATION:
? APPLICANT: MARASCO, WAYNE
? APPLICANT: HASSETLINE, WILLIAM
? TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
? TITLE OF INVENTION: PROTEINS
? NUMBER OF SEQUENCES: 78
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
? ADDRESSEE: CUSHMAN
? STREET: 130 WATER STREET
? CITY: BOSTON
? STATE: MASSACHUSETTS
? COUNTRY: US
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/438,190A
? FILING DATE:
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: EISENSTEIN, RONALD I.
? REGISTRATION NUMBER: 30628
? REFERENCE/DOCKET NUMBER: 41956
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617) 523-3400
? TELEFAX: (617) 523-6440
? TELEX: 200291 STRE UR
? INFORMATION FOR SEQ ID NO: 59:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 30 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? US-08-438-190A-59

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Query Match 81.4%; Score 11.4; DB 2; Length 30;
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14
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 Db 27 CCAGGTCAGTCCA 14

RESULT 15

US-08-803-085-14/c
 ; Sequence 14, Application US/08803085
 ; Patent No. 6011138

GENERAL INFORMATION:

APPLICANT: KLOETZER, William S.
 APPLICANT: NAKAMURA, Takehiko
 TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
 TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: P.O. Box 1404
 CITY: Alexandria
 STATE: Virginia
 COUNTRY: United States
 ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/803,085
 FILING DATE: 20-FEB-1997
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-353
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021

SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 14:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-803-085-14

Query Match 81.4%; Score 11.4; DB 3; Length 30;

Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGGTCAGNCCA 14
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 Db 30 CCAGGTCAGTCCA 17

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 Job time: 18.625 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 41.3438 seconds
(without alignments)
496.907 Million cell updates/sec

Title: US-09-964-666-14
Perfect score: 14
Sequence: 1 CAAGTCCAGNCA 14

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Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	13	92.9	14	10	US-09-964-666-14	Sequence 14, Appl
3	13	92.9	14	10	US-09-964-412-14	Sequence 14, Appl
4	12	85.7	24	9	US-09-940-185-281	Sequence 281, App
5	12	85.7	25	9	US-09-940-185-4261	Sequence 4261, App
6	11.4	81.4	17	9	US-10-211-357-44	Sequence 44, Appl
7	11.4	81.4	17	10	US-09-850-165-1	Sequence 1, Appl
8	11.4	81.4	18	9	US-10-067-790-16	Sequence 16, Appl
9	11.4	81.4	18	9	US-10-067-892-16	Sequence 16, Appl
10	11.4	81.4	18	9	US-09-539-383-16	Sequence 16, Appl
11	11.4	81.4	18	9	US-10-067-893-16	Sequence 16, Appl
12	11.4	81.4	20	9	US-10-024-018-2	Sequence 2, Appl
13	11.4	81.4	22	9	US-09-927-121B-38	Sequence 38, Appl
14	11.4	81.4	25	9	US-10-215-112-10872	Sequence 10872, A
15	11.4	81.4	26	10	US-09-211-357-13	Sequence 13, Appl
16	11.4	81.4	26	10	US-09-850-165-42	Sequence 42, Appl
17	11.4	81.4	30	9	US-10-103-666-14	Sequence 14, Appl
18	11.4	81.4	30	9	US-09-019-441-14	Sequence 14, Appl
19	11.4	81.4	35	9	US-09-825-805-218	Sequence 218, Appl

20	11.4	81.4	37	9	US-09-825-805-219	Sequence 219, App
21	11.4	81.4	38	9	US-09-925-664-52	Sequence 52, Appl
22	11.4	81.4	38	9	US-09-825-805-954	Sequence 954, App
23	11.4	81.4	38	9	US-09-825-805-987	Sequence 987, App
24	11.4	81.4	38	9	US-09-825-805-1106	Sequence 1106, App
25	11.4	81.4	38	9	US-09-930-423-2985	Sequence 2985, App
26	11.4	81.4	39	9	US-09-971-980-21	Sequence 21, Appl
27	11.4	81.4	39	9	US-09-971-980-21	Sequence 21, Appl
28	10.6	75.7	31	10	US-09-801-274-1163	Sequence 1163, App
29	10.4	74.3	17	9	US-09-864-636A-2609	Sequence 2609, App
30	10.4	74.3	20	9	US-10-087-323-19	Sequence 19, Appl
31	10.4	74.3	20	9	US-09-906-032A-3	Sequence 3, Appl
32	10.4	74.3	25	9	US-10-215-112-6573	Sequence 6573, App
33	10.4	74.3	25	9	US-10-208-731-10	Sequence 10, Appl
34	10.4	74.3	25	9	US-09-864-636A-2607	Sequence 2607, App
35	10.4	74.3	25	9	US-10-098-263B-35397	Sequence 35397, A
36	10.4	74.3	25	9	US-10-098-263B-35398	Sequence 35398, A
37	10.4	74.3	25	9	US-10-098-263B-35907	Sequence 35907, A
38	10.4	74.3	25	9	US-10-098-263B-51690	Sequence 51690, A
39	10.4	74.3	25	9	US-10-098-263B-57464	Sequence 57464, A
40	10.4	74.3	25	9	US-10-098-263B-59924	Sequence 59924, A
41	10.4	74.3	25	9	US-10-098-263B-62519	Sequence 62519, A
42	10.4	74.3	25	9	US-10-098-263B-62978	Sequence 62978, A
43	10.4	74.3	25	9	US-10-098-263B-81538	Sequence 81538, A
44	10.4	74.3	25	9	US-10-098-263B-89716	Sequence 89716, A
45	10.4	74.3	25	9	US-10-098-263B-102710	Sequence 102710, A

ALIGNMENTS

RESULT 1
US-09-964-667-14
Sequence 14, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Mands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-667-14

Query Match 92.9%; Score 13; DB 9; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGGTCCAGNCCA 14

DB 1 CAAGGTCCAGNCCA 14

RESULT 2

US-09-964-666-14

Sequence 14, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/964,666

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-666-14

QY 1 CAAGGTCCAGNCCA 14

DB 1 CAAGGTCCAGNCCA 14

RESULT 3

US-09-964-412-14

Sequence 14, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/964,412

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-964-412-14

QY 1 CAAGGTCCAGNCCA 14

DB 1 CAAGGTCCAGNCCA 14

RESULT 4

US-09-940-185-281/c

Sequence 281, Application US/09940185

Publication No. US20030096239A1

GENERAL INFORMATION:

APPLICANT: Chee, Mark

TITLE OF INVENTION: Probes and Decoder Oligonucleotides

FILE REFERENCE: A-69605-1

CURRENT APPLICATION NUMBER: US/09/940,185

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: US 60/227,948

PRIOR FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/228,854

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 4768

SOFTWARE: Patentin version 3.1

SEQ ID NO 281

LENGTH: 24

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Computer Generated Probe Sequence.

US-09-940-185-281

Query Match 85.7%; Score 12; DB 9; Length 24;

Best Local Similarity 92.3%; Pred. No. 1.8e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```
Publication No. US20030035807A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,790
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-790-16
```

Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 CAAGGTCAGNCCA 14
    1 |||||1111111
Db 15 CCAGGTCAGTCCA 2
```

```
RESULT 9
US-10-067-892-16/c
Sequence 16, Application US/10067892
Publication No. US20030039659A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,892
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-892-16
```

Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 CAAGGTCAGNCCA 14
    1 |||||1111111
Db 15 CCAGGTCAGTCCA 2
```

```
RESULT 10
US-09-539-382-16/c
Sequence 16, Application US/09539382
Publication No. US20030044417A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER
FILE REFERENCE: 18696-169195
CURRENT APPLICATION NUMBER: US/09/539,382
CURRENT FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-09-539-382-16
```

Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 CAAGGTCAGNCCA 14
    1 |||||1111111
Db 15 CCAGGTCAGTCCA 2
```

```
RESULT 11
US-10-067-893-16/c
Sequence 16, Application US/10067893
Publication No. US20030044420A1
GENERAL INFORMATION:
APPLICANT: MCCORMICK, Allison
APPLICANT: TUSE, Daniel
APPLICANT: REINL, Stephen
APPLICANT: LINDBO, John
APPLICANT: TURPEN, Thomas
TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER
FILE REFERENCE: 18696-169194
CURRENT APPLICATION NUMBER: US/10/067,893
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US/09/522,900
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: US 60/155,579
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: ()..()
OTHER INFORMATION: primer
US-10-067-893-16
```

Query Match 81.4%; Score 11.4; DB 9; Length 18;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 2; Indels 0; Gaps 0;

```
OY 1 CAAGGTCAGNCCA 14
```


CHROMOSOME/SEGMENT: VH1 leader sequence
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-211-357-13

Query Match 81.4%; Score 11.4; DB 9; Length 26;
Best Local Similarity 85.7%; Pred. No. 3.8e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CAAGSTCCAGNCCA 14
| | | | | | | | | |
DB 26 CCAGSTCCAGTCCA 13

Search completed: June 22, 2003, 03:18:25
Job time : 43.3438 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:28:37 ; Search time 604.734 Seconds
(without alignments)
374.936 Million cell updates/sec

Title: US-09-964-666-14

Sequence: 1 CAAGCTCCAGNCCA 14

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: EST:*
2: em_estbda:*
3: em_esthum:*
4: em_estinu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11.4	81.4	49	10	BE282036 601102010
2	11.4	81.4	50	10	AV428742 AV428742
3	11	78.6	50	14	H55190 H55190
4	10.4	74.3	19	17	A2825396 A2825396
5	10.4	74.3	31	17	A2437960 A2437960
6	10.4	74.3	46	13	B1908094 B1908094

C	7	10.4	74.3	50	9	AU107443
C	8	10	71.4	20	17	A2819886
C	9	10	71.4	34	9	AA669941
C	10	10	71.4	35	12	BF036425
C	11	10	71.4	42	17	T48919
C	12	10	71.4	44	17	A2489056
C	13	10	71.4	46	17	D86886
C	14	10	71.4	50	9	AU102541
C	15	10	71.4	50	9	AU102547
C	16	10	71.4	50	9	AU103657
C	17	10	71.4	50	9	AU105659
C	18	9.8	70.0	25	17	A2643950
C	19	9.8	70.0	28	17	A2327470
C	20	9.8	70.0	28	17	TA163A01P
C	21	9.8	70.0	29	17	A2492566
C	22	9.8	70.0	32	17	A2990287
C	23	9.8	70.0	32	17	TA130F07P
C	24	9.8	70.0	39	17	A2659162
C	25	9.8	70.0	40	9	AA880280
C	26	9.8	70.0	43	17	BH790549
C	27	9.8	70.0	47	13	BI221669
C	28	9.8	70.0	48	17	A2485794
C	29	9.8	70.0	49	9	AA876193
C	30	9.8	70.0	49	9	AA887238
C	31	9.8	70.0	49	9	A1457977
C	32	9.8	70.0	50	9	AU103167
C	33	9.8	70.0	50	9	AU106721
C	34	9.8	70.0	50	9	AU106942
C	35	9.8	70.0	50	14	N34794
C	36	9.4	67.1	22	17	A2389506
C	37	9.4	67.1	23	17	A2307822
C	38	9.4	67.1	23	17	A2480676
C	39	9.4	67.1	23	17	A2785457
C	40	9.4	67.1	32	17	A2456295
C	41	9.4	67.1	32	17	A2793160
C	42	9.4	67.1	33	17	A2791392
C	43	9.4	67.1	34	13	BJ034722
C	44	9.4	67.1	37	9	A1180523
C	45	9.4	67.1	37	9	A1815205

ALIGNMENTS

RESULT 1
BE282036/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BE282036 49 bp mRNA linear EST 26-OCT-2000
601102010F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:349431 5',
mRNA sequence.
BE282036
BE282036.1 GI:9157330
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerogonathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LIA6543 row: C column: 04
High quality sequence start: 2
High quality sequence stop: 49.
Location/Qualifiers

LOCUS	H55190	50 bp	mRNA	linear	EST 07-DEC-1995
DEFINITION	CHR220129 Chromosome 22 exon Homo sapiens cDNA Clone C22_166 5', mRNA sequence.				
ACCESSION	H55190				
VERSION	H55190.1	GI:1108056			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 50) Trofatter,J.A., Long,K.R., Murrell,J.R., Scotler,C.J., Gusella,J.F. and Buckler,A.J.				
TITLE	An expression-independent catalog of genes from human chromosome 22				
JOURNAL	Genome Res. 5 (3), 214-224 (1995)				
MEDLINE	96159527				
COMMENT	Contact: Buckler AJ Molecular Neurogenetics Unit Massachusetts General Hospital Building 149, 13th St., Charlestown MA 02129 Tel: 6177249616 Fax: 6177265736 Email: buckler@helix.mgh.harvard.edu Seq primer: T3.				
FEATURES	Location/Qualifiers				
source	1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="C22_166" /lab_host="E. coli DH5a" /clone_lib="Chromosome 22 exon" /note="Vector: pBluescriptRIKs+; Site_1: Sal I; Site_2: Bam HI (destroyed); Exons were isolated from human chromosome 22 specific cosmids using a modification of the method of exon amplification (Proc. Natl. Acad. Sci. USA 88:4005-4009, 1991). Amplified exons were digested with Sal I and Bgl II and subsequently cloned into pBluescriptRIKs+ at the Sal I and Bam HI sites."				
BASE COUNT	18 a 12 c 11 g . 9 t				
ORIGIN					
Query Match	78.6% Score 11; DB 14; Length 50;				
Best Local Similarity	91.7% Pred. No. 6.8e+04;				
Matches 11; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	3 AGGTCGAGNCCA 14 				
Db	29 AGGTCGAGACCA 40				
RESULT 4					
AZ825396/c	19 bp DNA linear GSS 20-FEB-2001				
LOCUS	2M0100N04R Mouse 10kb plasmid UNGC1M library Mus musculus genomic				
DEFINITION	clone UNGC2M0100N04 R, DNA sequence.				
ACCESSION	AZ825396				
VERSION	AZ825396.1	GI:12995304			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus				
AUTHORS	1 (bases 1 to 19) Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss.R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	plasmid inserts				
COMMENT	unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center				

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0100 row: N column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

1. 19
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG2M0100N04"
/clone_lib="Mouse 10kb plasmid library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

2 a 9 c 3 g 5 t

ORIGIN

Query Match 74.3%; Score 10.4; DB 17; Length 19;
Best Local Similarity 84.6%; Pred. No. 1.1e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAGGTCAGNCCA 14
||||| 11

DB 19 AAGGTCAGGCGCA 7

RESULT 5
AZ437960/c 31 bp DNA linear GSS 03-OCT-2000

LOCUS

DEFINITION 1M022614R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M022614 R, DNA sequence.

ACCESSION

AZ437960

VERSION

AZ437960.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: A column: 14
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 31.

FEATURES

source

Location/Qualifiers

1. 31
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M022614"
/clone_lib="Mouse 10kb plasmid library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

8 a 8 c 10 g 5 t

ORIGIN

Query Match 74.3%; Score 10.4; DB 17; Length 31;
Best Local Similarity 84.6%; Pred. No. 1.2e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 AAGGTCAGNCCA 14
||||| 11

DB 15 AAGGTCAGGCCA 3

RESULT 6
BI908094/c 46 bp mRNA linear EST 16-OCT-2001

LOCUS

DEFINITION 603067183F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5216252 5',
mRNA sequence.

ACCESSION

BI908094

VERSION

BI908094.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

Plate: LLAM11543 row: e column: 21

1. .46

Query Match	74.3%;	Score 10.4;	DB 13;	Length 46;
Best Local Similarity	84.6%;	Pred. No. 1.4e+05;		
Matches 11; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

RESULT 7
AU107443/c

LOCUS					
AI0107443		50 bp	mRNA	linear	EST 30-AUG-2000
DEFINITION	Sugano	Homo sapiens	CDNA library	Homo sapiens	CDNA clone
FEATURES	MELAN134NF, mRNA sequence.				

REFERENCE
AUTHORS

Eumariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata-

TITLE Mapping of mRNA start sites
 JOURNAL. Diverse transcriptional initiation revealed by fine, large-scale
 MEDLINE mapping of mRNA start sites
 COMMENT EMBO Rep. 2 (5), 388-393 (2001)
 Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8539, Japan
Email: yasukikie@ms.u-tokyo.ac.jp
Susuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Suganuma, S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. *Gene* 200 (1-2), 145-156 (1997).

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/organism="Homo sapiens"
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/clone="NBLAN134NF"
/clone_11b="Sugano Homo sapiens CDNA library"
/notes="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
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ORIGIN

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Db	44	AAGTCTGCCCA	32

AZ819886 20 bp DNA linear C55 20-FPB-2001

LOCUS	A2013660	20 bp	DNA	linear	055 20-FEB-2000
DEFINITION	M00051H16R Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGC2M0091H16 R, DNA sequence.				
ACCESSION	A2010886				

ACCESSION	Z6819000	
VERSION	AZ6819886.1	GI:12989794
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	

REFERENCE
AUTHORS
TITLE

Eukariota; Metazoa; Crustacea; Crustacea; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT
Unpublished (2000)
Contact: Robert B. Weiss

University of Utah genome center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0091 row: H column: 16
Seq primer: CACACAGCGAACAACGTAAGACC
Class: plasmid ends
High quality sequence stop 20. -

FEATURES
Source

BASE COUNT
RIGIN

7 a 3 c 4 g 6 t

/organism="Mus musculus"
/strain="C57BL/6J"
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/clone="UUC2M0091H16"
/clone_lib="Mouse 10kb plasmid UUC2M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/nanres/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[9]AE129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query match	71.48; Score 10; DB 17; Length 20
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TITLE Direct Submission
JOURNAL Submitted (01-AUG-1996) Miki Ohira, Kazusa DNA Research Institute,
Laboratory of Gene Structure 1: 1532-3 Yanaubino, Kisarazu, Chiba
292, Japan (E-mail: oohira@kazusa.or.jp, Tel: +81-438-52-3932,
Fax: +81-438-52-3931)

FEATURES
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BASE COUNT
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exon

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Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCCAG 10
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17 CAAGTCCAG 8

Db

RESULT 14
AUI02541 50 bp mRNA linear EST 30-AUG-2001

LOCUS AUI02541
DEFINITION AUI02541 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
HRC07574, mRNA sequence.
ACCESSION AUI02541
VERSION AUI02541.1 GI:13552062
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
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/organism="Homo sapiens"
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/clone="HRC07574"
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dimethylfumarate treated u937 cells"

BASE COUNT
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ORIGIN

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Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||
3 GGTCCAGTCCA 13

Db

RESULT 15
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LOCUS AUI02547
DEFINITION AUI02547 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
W1000, mRNA sequence.
ACCESSION AUI02547
VERSION AUI02547.1 GI:13552068
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. .50
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/note="Differential display comparison of untreated and
dimethylfumarate treated u937 cells"

BASE COUNT
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ORIGIN

Query Match 71.4%; Score 10; DB 9; Length 50;
Best Local Similarity 90.9%; Pred. No. 2.3e+05;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 GGTCCAGTCCA 11

Db

Search completed: June 21, 2003, 23:59:12
Job time : 609.901 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:23:11 ; Search time 602.344 seconds

(without alignments)
1449.478 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCAATCTGTGGTAAGAGTGGACACCTGTG 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
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28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rod:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	19.6	65.3	49	9	HUMD2H04M3	D17183 Human HepG2
2	15.8	52.7	31	6	AR051493	AR051493 Sequence
3	15.8	52.7	31	6	AR072633	AR072633 Sequence
4	15.8	52.7	31	6	AR073178	AR073178 Sequence
5	15.6	52.0	47	6	AX114379	AX114379 Sequence
6	15.4	51.3	29	6	AX411689	AX411689 Sequence
7	15.4	51.3	29	6	AX411691	AX411691 Sequence
8	15.2	50.7	38	6	AX056763	AX056763 Sequence
9	14.8	49.3	22	6	AX466859	AX466859 Sequence
10	14.8	49.3	31	6	AX247929	AX247929 Sequence
11	14.8	49.3	38	6	AX056759	AX056759 Sequence
12	14.8	49.3	39	6	I44807	I44807 Sequence 31
13	14.8	49.3	42	6	I44804	I44804 Sequence 28
14	14.8	49.3	50	10	AR071670	AR071670 Mus muscu
15	14.4	48.0	30	6	AX338660	AX338660 Sequence
16	14.2	47.3	36	6	E27466	E27466 Novel gene
17	14.2	47.3	39	6	AX044055	AX044055 Sequence
18	14.2	47.3	39	6	AX044109	AX044109 Sequence
19	14.2	47.3	39	6	AX044157	AX044157 Sequence
20	14.2	47.3	39	6	AX134391	AX134391 Sequence
21	14.2	47.3	40	6	AX068155	AX068155 Sequence
22	14.2	47.3	42	6	A93509	A93509 Sequence 12
23	14.2	47.3	48	6	A93513	A93513 Sequence 6
24	14.2	47.3	48	6	A93514	A93514 Sequence 7
25	14.2	47.3	24	6	AX290680	AX290680 Sequence
26	14.2	46.7	36	9	HUMTCGVJ39	L39506 Homo sapien
27	14.2	46.7	36	9	HUMTCRDAAD	M64421 Human T cel
28	14.2	46.7	46	6	AR023959	AR023959 Sequence
29	14.2	46.7	46	6	I15460	I15460 Sequence 38
30	14.2	46.7	47	6	AX378324	AX378324 Sequence
31	14.2	46.7	47	6	AX378746	AX378746 Sequence
32	13.8	46.0	26	6	AR091186	AR091186 Sequence
33	13.8	46.0	26	6	AR198221	AR198221 Sequence
34	13.8	46.0	31	6	AX248794	AX248794 Sequence
35	13.8	46.0	35	6	E13897	E13897 PCR primer
36	13.8	46.0	43	6	A45335	A45335 Sequence 5
37	13.8	46.0	43	6	AR061140	AR061140 Sequence
38	13.8	46.0	43	9	HSARWG1A3	X75551 H.sapiens (
39	13.6	45.3	36	6	AX247486	AX247486 Sequence
40	13.4	44.7	24	6	A05412	A05412 Synthetic O
41	13.4	44.7	24	6	A09619	A09619 Oligonucleo
42	13.4	44.7	29	6	E13339	E13339 Probe. 4/19
43	13.4	44.7	40	6	AR059136	AR059136 Sequence
44	13.4	44.7	40	6	AR169562	AR169562 Sequence
45	13.4	44.7	50	6	AR032714	AR032714 Sequence

ALIGNMENTS

RESULT 1
LOCUS HUMD2H04M3 49 bp mRNA linear PRI 04-FEB-1999
DEFINITION Human HepG2 3' region Mbol cDNA, clone hmd2h04m3.
ACCESSION D17183
VERSION D17183.1 GI:598688
KEYWORDS gene signature.
SOURCE Homo sapiens
ORGANISM Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_hib:Kisefu.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 49)
TITLE The addition of 5'-coding information to a 3'-directed cDNA library
Improves analysis of gene expression

JOURNAL Gene 146 (2), 199-207 (1994)
MEDLINE 94357437
REFERENCE 2 (bases 1 to 49)
AUTHORS Matoba,R.
TITLE Direct Submission
JOURNAL Submitted (21-Jul-1993) Ryo Matoba, Osaka University, Institute for Molecular and Cellular Bio; 1-3, Yamada-Oka, Suita, Osaka 565,
Japan (E-mail:matoba@inherit.limb.osaka-u.ac.jp,
Tel:81-6-877-5111(x 3314), Fax:81-6-877-1922)
Submitted (21-Jul-1993) to DDBJ by:
Ryo Matoba
Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2
Kizugawada Kizu-cyo,
Soraku-gun, Kyoto
Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321.
Location/Qualifiers

FEATURES
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/sex="Male"
/cell_line="HepG2"
/clone_1ib="Kiseru"

BASE COUNT 13 a 15 c 12 g 9 t
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Query Match 65.3%; Score 19.6; DB 9; Length 49;
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Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAAGTGGACACCT 26
17 TTCACCTGGGTGACAGAGTACACACC 42
Db

RESULT 2
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LOCUS AR051493 31 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 63 from patent US 5830670.
ACCESSION AR051493
VERSION AR051493.1 GI:5974857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5830670-A 63 03-NOV-1998;
FEATURES
source 1..31
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Location/Qualifiers

BASE COUNT 6 a 10 c 8 g 7 t
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Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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LOCUS AR072633 31 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 63 from patent US 5948634.
ACCESSION AR072633
VERSION AR072633.1 GI:9999397

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948634-A 63 07-SEP-1999;
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Location/Qualifiers

BASE COUNT 6 a 10 c 8 g 7 t
ORIGIN

Query Match 52.7%; Score 15.8; DB 6; Length 31;
Best Local Similarity 74.1%; Pred. No. 2.1e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db

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LOCUS AR073178 31 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 63 from patent US 5948888.
ACCESSION AR073178
VERSION AR073178.1 GI:9999941
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 31)
AUTHORS de la Monte,S. and Wands,J.R.
TITLE Neural thread protein gene expression and detection of Alzheimer's disease
JOURNAL Patent: US 5948888-A 63 07-SEP-1999;
FEATURES
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/organism="unknown"
Location/Qualifiers

BASE COUNT 6 a 10 c 8 g 7 t
ORIGIN

Query Match 52.7%; Score 15.8; DB 6; Length 31;
Best Local Similarity 74.1%; Pred. No. 2.1e+04;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCCTGGGTAAAGTGGACACCT 27
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Db

RESULT 5
AX114379
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DEFINITION Sequence 48 from Patent WO0129257.
ACCESSION AX114379
VERSION AX114379.1 GI:14031343
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Schork,N. and Skierczynski,B.
TITLE Methods of genetic cluster analysis and use thereof
JOURNAL Patent: WO 0129257-A 48 26-APR-2001;
GENSET (FR)
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RESULT 10	AX247929	31 bp	DNA	linear	PAT 28-SEP-2001
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ACCESSION	AX247929				
VERSION	AX247929.1	GI:15862552			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 31)				
AUTHORS	Cargill,M., Ireland,J.S. and Lander,E.S.				
TITLE	Human single nucleotide polymorphisms				
JOURNAL	Patent: WO 0166800-A 8 13-SEP-2001;				
	WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)				
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Matches	19; Conservative 1; Mismatches 8;			Indels 0; Gaps 0;	
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	:				
Db	2 CATCAAGGATGAATGTGACACCTGCG 29				
RESULT 11	AX056759	38 bp	DNA	linear	PAT 17-JAN-2001
LOCUS	AX056759				
DEFINITION	Sequence 25 from Patent WO075319.				
ACCESSION	AX056759				
VERSION	AX056759.1	GI:12309735			
KEYWORDS					
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
	artificial sequences.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Papadopoulos,N.D., Davis,S. and Yancopoulos,G.D.				
TITLE	Modified chimeric polypeptides with improved pharmacokinetic properties				
JOURNAL	Patent: WO 0075319-A 25 14-DEC-2000;				
	REGENERON PHARMACEUTICALS, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..38				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
	/note="primer"				
BASE COUNT	8 a 6 c 10 g 14 t				
ORIGIN					
Query Match	49.3%; Score 14.8; DB 6;			Length 38;	
Best Local Similarity	73.1%; Pred. No. 6.1e+04;				
Matches	19; Conservative 0; Mismatches 7;			Indels 0; Gaps 0;	
QY	5 TCCTGGCTAAGATGGACACCTGTG 30				
Db	2 TCCTGGCACACGCTGATATCTATG 27				
RESULT 12	I44807/c	39 bp	DNA	linear	PAT 07-OCT-1997
LOCUS	I44807				
DEFINITION	Sequence 31 from patent US 5635599.				
ACCESSION	I44807				
VERSION	I44807.1	GI:2469520			
KEYWORDS					

SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 39)
TITLE	Pastan,I.H., Kreltman,R.J. and Puri,R.K.
JOURNAL	Fusion proteins comprising circularly permuted ligands
FEATURES	Patent: US 5635599-A 31 03-JUN-1997; Location/Qualifiers
SOURCE	1..39 /organism="unknown"
BASE COUNT	7 a 10 c 12 g 10 t
ORIGIN	
Query Match	49.3% Score 14.8; DB 6; Length 39;
Best Local Similarity	73.1% Pred. No. 6.1e+04;
Matches	19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	2 TCATCCTGTGCTAAGAGTGGGACACCT 27 26 TCACCGGAGGTACGCTGGGGCACCCT 1
RESULT 13	
LOCUS	I44804 42 bp DNA Linear PAT 07-OCT-1997
DEFINITION	Sequence 28 from patent US 5635599.
ACCESSION	I44804
VERSION	I44804.1 GI:2469517
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 42)
TITLE	Pastan,I.H., Kreltman,R.J. and Puri,R.K.
JOURNAL	Fusion proteins comprising circularly permuted ligands
FEATURES	Patent: US 5635599-A 28 03-JUN-1997; Location/Qualifiers
SOURCE	1..42 /organism="unknown"
BASE COUNT	10 a 12 c 11 g 9 t
ORIGIN	
Query Match	49.3% Score 14.8; DB 6; Length 42;
Best Local Similarity	73.1% Pred. No. 6e+04; 7; Indels 0; Gaps 0;
Matches	19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY	2 TCATCCTGTGCTAAGAGTGGGACACCT 27 5 TCACCGGAGGTACGCTGGGGCACCCT 30
DB	
RESULT 14	
LOCUS	AF071670 50 bp DNA linear ROD 26-JAN-1999
DEFINITION	Mus musculus clone MPJ-09. Immunoglobulin heavy chain D-J region
ACCESSION	AF071670
VERSION	AF071670.1 GI:3320527
KEYWORDS	
SOURCE	Mus musculus.
ORGANISM	Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 50)
TITLE	Klonowski,K.D., Primiano,L.L. and Monestier,M.
JOURNAL	Atypical VH-D-JH rearrangements in newborn autoimmune MRL mice
MEDLINE	J. Immunol. 162 (3), 1566-1572 (1999)
PUBMED	99138837
REFERENCE	9973414
AUTHORS	2 (bases 1 to 50)
TITLE	Monestier,M. and Klonowski,K.
JOURNAL	Direct Submission
Submitted (12-JUN-1998)	Microbiology and Immunology, Temple

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OM nucleic acid search, using sw model

Run on: June 21, 2003, 21:23:51 ; Search time 164.531 Seconds
(without alignments)
410.621 Million cell updates/sec

Title: US-09-964-666-9
Perfect score: 30
Sequence: 1 TTCACTCCGTGGTAAGATGGGACACCTCTG 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
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18: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
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20: /SID2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.6	55.3	24	ABA05479	Human RNA gyrase 1
C 2	16.2	54.0	24	ABN89564	Human uracil monon
C 3	16	53.3	47	AA266299	Human map-related
C 4	16	53.3	47	AA266299	Human map-related
C 5	16	53.3	50	AA266299	Human map-related
C 6	15.4	51.3	29	AA266299	Human gene signatu
C 7	15.4	51.3	29	AA266299	Human gene signatu
C 8	15.2	50.7	38	AA266299	Human IGS43 GPCR D
C 9	15.2	50.7	45	AA266299	PCR primer F11D2.
					Upstream45 primer

10	14.8	49.3	22	24	ABL2859	G protein-coupled
11	14.8	49.3	38	22	AAA91083	PCR primer F11D2.
12	14.8	49.3	39	16	AA266299	Amplification prim
13	14.8	49.3	42	16	AA266299	Amplification prim
C 14	14.6	48.7	24	22	AAH7680	Human tyrosinase 1
C 15	14.6	48.7	33	21	AAA88764	Respiratory syncyt
C 16	14.6	48.7	45	21	AAA07136	S. pyogenes cystei
C 17	14.4	48.0	30	22	AAH27041	Interleukin 10 rec
C 18	14.4	48.0	47	21	AA266299	Human map-related
C 19	14.4	48.0	49	22	AAK65337	Human immune/haema
C 20	14.4	48.0	49	22	AAI62905	Human genomic DNA
C 21	14.2	47.3	36	20	AAH88249	Human CRT-1 DNA pr
C 22	14.2	47.3	39	21	AAH88249	Rice BPSs PCR pri
C 23	14.2	47.3	39	21	AAH88249	Rice BPSs PCR pri
C 24	14.2	47.3	39	21	AAH88249	Rice BPSs PCR pri
C 25	14.2	47.3	39	21	AAH88249	Rice BPSs PCR pri
C 26	14.2	47.3	40	22	AAH88249	Human novel melast
C 27	14.2	47.3	41	19	AAV50841	Chicken insulator
C 28	14.2	47.3	41	19	AAV50841	Brassica sp. polym
C 29	14.2	47.3	41	19	AAV50841	Brassica sp. polym
C 30	14.2	47.3	41	24	AAO77609	Human glutamate re
C 31	14.2	47.3	48	18	AAH88249	Feline parvoviral
C 32	14.2	47.3	24	24	AAH88249	Human cell divisio
C 33	14.2	47.3	24	24	AAH88249	Capture oligonucle
C 34	14.2	47.3	24	24	AAH88249	Capture oligonucle
C 35	14.2	47.3	27	19	AAV33786	Human tyrosinase 1
C 36	14.2	47.3	27	19	AAV33786	Integrin beta-1 ch
C 37	14.2	47.3	28	24	AAH88249	PCR primer of the
C 38	14.2	47.3	28	24	AAH88249	M30 protein vector
C 39	14.2	47.3	41	24	AAH88249	Human alpha 2,3-si
C 40	14.2	47.3	46	13	AAO24360	Oligonucleotide pri
C 41	14.2	47.3	47	24	AAH88249	Human obesity-asso
C 42	13.8	46.0	26	24	AAH88249	Human US2 gene bi
C 43	13.8	46.0	31	20	AAH88249	Human gene specifi
C 44	13.8	46.0	31	22	AAH88249	Human biologic po
C 45	13.8	46.0	35	18	AAH88249	Human single nucle
						Human genomic EMBL

ALIGNMENTS

RESULT 1	ABA05479/c	standard; DNA; 24 BP.
ID	ABA05479	
AC	ABA05479	
XX		
XX		
DT	01-MAR-2002	(first entry)
XX		
DE	Human RNA gyrase 12 PCR primer SEQ ID NO 4.	
XX		
KW	Human: RNA gyrase 12; malignant tumour; haemopathy; HIV; infection;	
KW	Human immunodeficiency virus; immunological disease; inflammation;	
KW	enzyme; PCR primer; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	CN1311325-A.	
XX		
PD	05-SEP-2001.	
XX		
PF	02-MAR-2000; 2000CN-0111862.	
XX		
PR	02-MAR-2000; 2000CN-0111862.	
XX		
PA	(BODE-) BODE GENE DEV CO LTD SHANGHAI.	
XX		
PI	Mao Y, Xie Y;	
XX		
DR	WPI: 2002-049927/07.	
XX		
PT	New polypeptide-human RNA unwindase 12 and polynucleotide encoding the	
PT	polypeptide -	

```
XX Example 2; Page 17 (Disclosure): 33pp; Chinese.
PS
CC The invention relates to human RNA gyrase 12, the polynucleotide encoding
CC this polypeptide and DNA recombinant techniques to produce this
CC polypeptide. The present invention also discloses a method of applying
CC this polypeptide to treat various diseases, such as malignant tumour,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammations. The present sequence is that of a PCR primer, useful to
CC the invention.
XX
SQ Sequence 24 BP; 3 A; 10 C; 6 G; 5 T; 0 other:
Query Match 55.3%; Score 16.6; DB 24; Length 24;
Best Local Similarity 82.6%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 ATCTGGGTAAAGTGGACACC 26
DB 24 AGCTGGGTGAGAGTGACACCC 2

RESULT 2
ABN89564/c
ID ABN89564 standard; DNA; 24 BP.
XX
AC ABN89564;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human uracil mononucleotide synthetase 9.9 PCR primer 2 SEQ ID NO:4.
XX
KW Human; uracil mononucleotide synthetase 9.9; enzyme; PCR primer; ss.
XX
OS Homo sapiens.
XX
PM CN1333341-A.
XX
PD 30-JAN-2002.
XX
PF 07-JUL-2000; 2000CN-0117079.
XX
PR 07-JUL-2000; 2000CN-0117079.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI: 2002-340719/38.
XX
PT A human uracil mononucleotide synthetase 9.9 polypeptide, and the
XX polynucleotide encoding it, for treating various diseases -
XX
PS Example 2; Page 16 (Disclosure): 34pp; Chinese.
XX
CC The present invention describes human uracil mononucleotide synthetase
CC 9.9 (I). Also described is a process for producing (I) using DNA
CC recombination technology. (I) and the polynucleotide encoding it
CC can be used in the treatment of various diseases. The present sequence
CC represents a PCR primer for (I), which is used in an example from the
CC present invention.
XX
SQ Sequence 24 BP; 4 A; 9 C; 6 G; 5 T; 0 other:
Query Match 54.0%; Score 16.2; DB 24; Length 24;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 CCTGGTAGAGTGGACACC 26
DB 23 CCTGGCAAGAGTGACATCC 3
```

```
RESULT 3
AAZ66299
ID AAZ66299 standard; DNA; 47 BP.
XX
AC AAZ66299;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:646.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(24,C)
FT /*tag=
FT /standard_name="single nucleotide polymorphism"
XX
PN WO954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-1B00822.
XX
PR 21-APR-1998; 98US-0082614.
XX
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
XX map of the human genome -
XX
PS Claim 1; Page 368; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ6579 to AAZ7740 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 14 C; 8 G; 9 T; 0 other:
Query Match 53.3%; Score 16; DB 21; Length 47;
Best Local Similarity 79.2%; Pred. No. 8.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 CATCTGGCTAAGAGTGACACC 26
DB 10 CATCTGGCTAAGAGTGACACC 33

RESULT 4
AAF89248
ID AAF89248 standard; DNA; 47 BP.
```

XX	AA89248;
AC	
XX	10-DEC-2001 (first entry)
DT	
XX	
DE	Sample member clustering method related human polymorphic site #48.
XX	
XX	Cluster: hierarchical clustering algorithm; population based study;
KW	clinical trial; DNA fingerprint; genetic profile analysis; PCR primer;
RW	SNP; single nucleotide polymorphism; ss.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	allele
FT	Location/Qualifiers
FT	replace(24,C)
FT	/*tag= a
XX	
PN	WO200129257-A2.
XX	
PD	26-APR-2001.
XX	
PE	20-OCT-2000; 2000WO-IB01632.
XX	
PR	22-OCT-1999; 99US-0161231.
PR	07-JUL-2000; 2000US-0216897.
XX	
PA	(GEST) GENSET.
PI	Schorf N, Skierczynski B;
XX	
DR	WPI: 2001-316248/33.
XX	
PT	Genetic clustering by distributing members into optimal numbers of
PT	clusters determined by a hierarchical clustering algorithm or by
PT	paired-pair analysis of homozygous pairs in clusters got from
PT	non-hierarchical clustering
XX	
PS	Claim 61; Page 71; 100pp; English.
XX	
CC	The present invention describes methods of clustering members of a
CC	sample, involving applying a hierarchical clustering algorithm to the
CC	sample members, determining the optimal number of clusters based on this
CC	clustering. The methods are useful in population based studies such as
CC	clinical trials, DNA fingerprinting and genetic profile analyses. The
CC	present sequence was used to demonstrate the method of the invention.
XX	
XX	Sequence 47 BP; 16 A; 14 C; 8 G; 9 T; 0 other;
XX	
Query Match	53.3%; Score 16; DB 22; Length 47;
Best Local Similarity	79.2%; Pred. No. 8.9e+02;
Matches 19;	Conservative 0; Mismatches 5; Indels 0; Gaps 0;
XX	
0Y	3 CATCCTGGGTAAGAGTGGGACACC 26
	11111111111111111111
Db	10 CATCCTGGCTAACAGAGTGAAC 33
	11111111111111111111
XX	
RESULT 5	
AA725713	
ID	AA725713 standard; cDNA to mRNA; 50 BP.
XX	
AC	AA725713;
XX	
DT	10-OCT-1996 (first entry)
XX	
DE	Human gene signature HMG507919.
XX	
KW	gene signature; messenger RNA; mRNA; relative abundance; frequency;
RW	human; cloning; mapping; non-biased library; diagnosis; detection;
KW	cell typing; abnormal cell function; ss.
OS	Homo sapiens

P0
PN W09514772-A1.
XX 01-JUN-1995.
PD XX
PE 11-NOV-1994; 94MO-JP01916.
PR 12-NOV-1993; 93JP-0355504.
PS (MATS/) MATSUBARA K.
PT (OKUB/) OKUBO K.
XX Matsubara K, Okubo K;
PI MPI; 1995-206931/27.
DR
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT for diagnosis of abnormal cell function. By preparing cDNA that
PT reflects relative abundance of corresp. mRNA in specific human
PT tissues

Claim 1: Page 1912: 2245pp: Japanese.

A single-stranded DNA (or its complementary strand or the corresp.
double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in AAT19001-TG6837 and which is able to hybridize to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed cDNA libraries prepared
from various human tissues; synthesis of cDNA was initiated from the
3' end of mRNA by using poly(T) as the sole primer. Since the 3'-
untranslated sequence is unique to a particular RNA species, almost
all the 3'-oriented CDNA's hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.

Sequence 50 BP; 12 A; 13 C; 12 G; 12 T; 1 other;

Query Match 53.3%; Score 16; DB 16; Length 50;
Best Local Similarity 76.0%; Pred. No. 8.ge+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 TTCTCCGTGGTAAAGACGGGCACC 25
| | | ||||| | | | | |
DB 17 TCCTCAGNCCTGGTTAACAGTCGACTC 41

RESULT 6
AADJ1162/C
ID AADJ1162 standard; DNA: 29 BP.
XX
AC AADJ1162;
XX
DT 27-AUG-2002 (first entry)

Primer IP14924 for cloning human IGS43 GPCR cDNA.

IGS43: G-protein coupled receptor; GPCR; uterus; lung; trachea;
colon; small intestine; stomach; mammary gland; prostate; testis;
psychiatric disorder; central nervous system disorder; schizophrenia;
episodic and paroxysmal anxiety disorder; Parkinson's disease;
multiple sclerosis; Alzheimer's disease; cardiovascular disease;
heart failure; angina pectoris; kidney disease; dyslipidaemias; obesity;
emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes;
osteoporosis; inflammation; infection; human immunodeficiency virus; HIV;
cancer; immune disorder; urinary retention; asthma; allergy; arthritis;
benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy;
gynaecological disorder; vaccine; human; PCR primer; ss.
XX Homo sapiens
OS

XX WO200228897-A2.
 PN 11-APR-2002.
 XX 28-SEP-2001; 2001WO-EP11319.
 XX 02-OCT-2000; 2000EP-0203411.
 PR 04-OCT-2000; 2000US-237394P.
 XX (SOLV) SOLVAY PHARM BV.
 PA Deleersnijder W, Blockx H, De Moor L;
 PI WPI; 2002-426102/45.
 DR Novel G-protein coupled receptor, termed IGS43 polypeptide and nucleic
 PT acid encoding the polypeptide, useful for treating disorders of uterus,
 PT kidney, lung, colon, stomach, mammary gland, prostate and testis -
 XX Example 1; Page 33; 59pp; English.

XX The invention relates to IGS43 G-protein coupled receptor (GPCR) and the
 CC polynucleotide encoding it. The IGS43 polypeptide, polynucleotide,
 CC agonist, antagonist or antibody is useful for treating dysfunctions or
 CC disorders related to uterus, kidney, lung, trachea, colon, small
 CC intestine, stomach, mammary gland, prostate, testis, central nervous
 CC system, cerebellum and spinal cord. The polypeptide is useful as vaccine
 CC for inducing immunological response in a mammal, for treating
 CC psychiatric and central nervous system disorders including
 CC schizophrenia, episodic and paroxysmal anxiety disorders e.g. obsessive
 CC compulsive disorder, post traumatic disorder, phobia and panic, major
 CC depressive disorder, bipolar disorder, Parkinson's disease, general
 CC anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer's
 CC disease, dementia, severe mental retardation, Huntington's disease,
 CC dyskinesias, Tourette's syndrome, tics, tremor, dystonia, spasms,
 CC anorexia, bulimia, stroke, addiction/dependency/craving, sleep
 CC disorder, epilepsy, migraine, attention deficit/hyperactivity disorder,
 CC cardiovascular diseases including heart failure, angina pectoris,
 CC arrhythmias, myocardial infarction, cardiac hypertrophy, hypertension,
 CC hypertension, thrombosis, arteriosclerosis, cerebral vasospasm,
 CC subarachnoid haemorrhage, cerebral ischaemia, cerebral infarction,
 CC peripheral vascular disease, Raynaud's disease, kidney disease,
 CC dyslipidaemias, obesity, emesis, gastrointestinal disorders including
 CC irritable bowel syndrome, inflammatory bowel disease, diabetic
 CC gastroparesis and diabetes, ulcers, diarrhoea, osteoporosis,
 CC inflammations, infections including bacterial, fungal, protozoan and
 CC viral infections, particularly human immunodeficiency virus (HIV)-1 or
 CC HIV-2 infections, pain, cancers, chemotherapy induced injury, tumour
 CC invasion, immune disorders, urinary retention, asthma, allergies,
 CC arthritis, benign prostatic hypertrophy, endotoxin shock, sepsis,
 CC complications of diabetes mellitus, and gynaecological disorders.
 CC The polypeptide and polynucleotide of the invention are also useful as
 CC research reagents and materials for discovery of treatments and
 CC diagnostics to animal and human diseases. The polynucleotide is
 CC also useful for chromosome identification. The polypeptide is also useful
 CC for assessing the binding of small molecule substrates and ligands in
 CC cells, cell-free preparations, chemical libraries and natural product
 CC mixtures. The present sequence is a PCR primer used for cloning human
 CC IGS43 GPCR cDNA.

XX Sequence 29 BP; 5 A; 10 C; 6 G; 8 T; 0 other:

XX Query Match 51.3% Score 15.4; DB 24; Length 29;
 XX Best Local Similarity 94.1% Pred. No. 1.6e+03;
 XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AGAGTGGACACCTGTG 30
 DB 27 AGAGAGGACACCTGTG 11

RESULT 7

AD31164/C
 ID AAD31164 standard; DNA; 29 BP.
 XX AAD31164;
 XX 27-AUG-2002 (first entry)
 XX Human IGS43 GPCR DNA amplifying primer IP15332.
 DE IGS43; G-protein coupled receptor; GPCR; uterus; lung; trachea;
 KW colon; small intestine; stomach; mammary gland; prostate; testis;
 KW psychiatric disorder; central nervous system disorder; schizophrenia;
 KW episodic and paroxysmal anxiety disorder; Parkinson's disease;
 KW multiple sclerosis; Alzheimer's disease; cardiovascular disease;
 KW heart failure; angina pectoris; kidney disease; dyslipidaemias; obesity;
 KW emesis; gastrointestinal disorder; inflammatory bowel disease; diabetes;
 KW osteoporosis; inflammation; infection; human immunodeficiency virus; HIV;
 KW cancer; immune disorder; urinary retention; asthma; allergy; arthritis;
 KW benign prostatic hypertrophy; endotoxin shock; sepsis; gene therapy;
 KW gynaecological disorder; vaccine; human; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO200228897-A2.
 PN 11-APR-2002.
 XX 28-SEP-2001; 2001WO-EP11319.
 XX 02-OCT-2000; 2000EP-0203411.
 PR 04-OCT-2000; 2000US-237394P.
 XX (SOLV) SOLVAY PHARM BV.
 PA Deleersnijder W, Blockx H, De Moor L;
 PI WPI; 2002-426102/45.
 DR Novel G-protein coupled receptor, termed IGS43 polypeptide and nucleic
 PT acid encoding the polypeptide, useful for treating disorders of uterus,
 PT kidney, lung, colon, stomach, mammary gland, prostate and testis -
 XX Example 2; Page 36; 59pp; English.

XX The invention relates to IGS43 G-protein coupled receptor (GPCR) and the
 CC polynucleotide encoding it. The IGS43 polypeptide, polynucleotide,
 CC agonist, antagonist or antibody is useful for treating dysfunctions or
 CC disorders related to uterus, kidney, lung, trachea, colon, small
 CC intestine, stomach, mammary gland, prostate, testis, central nervous
 CC system, cerebellum and spinal cord. The polypeptide is useful as vaccine
 CC for inducing immunological response in a mammal, for treating
 CC psychiatric and central nervous system disorders including
 CC schizophrenia, episodic and paroxysmal anxiety disorders e.g. obsessive
 CC compulsive disorder, post traumatic disorder, phobia and panic, major
 CC depressive disorder, bipolar disorder, Parkinson's disease, general
 CC anxiety disorder, autism, delirium, multiple sclerosis, Alzheimer's
 CC disease, dementia, severe mental retardation, Huntington's disease,
 CC dyskinesias, Tourette's syndrome, tics, tremor, dystonia, spasms,
 CC anorexia, bulimia, stroke, addiction/dependency/craving, sleep
 CC disorder, epilepsy, migraine, attention deficit/hyperactivity disorder,
 CC cardiovascular diseases including heart failure, angina pectoris,
 CC arrhythmias, myocardial infarction, cardiac hypertrophy, hypertension,
 CC hypertension, thrombosis, arteriosclerosis, cerebral vasospasm,
 CC subarachnoid haemorrhage, cerebral ischaemia, cerebral infarction,
 CC peripheral vascular disease, Raynaud's disease, kidney disease,
 CC dyslipidaemias, obesity, emesis, gastrointestinal disorders including
 CC irritable bowel syndrome, inflammatory bowel disease, diabetic
 CC gastroparesis and diabetes, ulcers, diarrhoea, osteoporosis,
 CC inflammations, infections including bacterial, fungal, protozoan and
 CC viral infections, particularly human immunodeficiency virus (HIV)-1 or
 CC HIV-2 infections, pain, cancers, chemotherapy induced injury, tumour
 CC invasion, immune disorders, urinary retention, asthma, allergies,
 CC arthritis, benign prostatic hypertrophy, endotoxin shock, sepsis,

CC complications of diabetes mellitus, and gynaecological disorders.
CC The polypeptide and polynucleotide of the invention are also useful as
CC research reagents and materials for discovery of treatments and
CC diagnostics to animal and human diseases. The polynucleotide is
CC also useful for chromosome identification. The polypeptide is also useful
CC for assessing the binding of small molecule substrates and ligands in
CC cells, cell-free preparations, chemical libraries and natural product
CC mixtures. The present sequence is a PCR primer used for amplifying human
CC IGS43 GPCR DNA.
XX
SQ Sequence 29 BP; 4 A; 10 C; 8 G; 7 T; 0 other;

Query Match 51.3%; Score 15.4; DB 24; Length 29;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 14 AGAGTGGGACACCTGTG 30
DB 27 AGAGAGGGACACCTGTG 11

RESULT 8

AAA91086/C
ID AAA91086 standard; DNA; 38 BP.

AC AAA91086;

DT 05-APR-2001; (first entry)

DE PCR primer F11D2.VEGFR3D3.s for F11l receptor fusion DNA sequence.

KW F11l receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.

OS Unidentified.

PN WO200075319-A1.

PD 14-DEC-2000;

PF 23-MAY-2000; 2000WO-US14142.

PR 08-JUN-1999; 99US-0138133.

PA (REGG-) REGENERON PHARM INC.

PI Papadopoulos NJ, Davis S, Yancopoulos GD;

DR WPI; 2001-071076/08.

PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
PT and its fragments, useful for diagnosis, evaluation, and treatment of
PT diseases associated with the gene expression and for producing model
PT systems -

XX Example 17; Page 63; 159pp; English.

CC This sequence represents a PCR primer used to construct DNA
CC sequences encoding the fusion proteins of the invention between
CC the F11l receptor and the Fc region of IgG. The specification relates
CC to modified chimeric polypeptides with improved pharmacokinetics. The
CC modified chimeric polypeptides are preferably F11l receptor polypeptides
CC that have been modified to improve their pharmacokinetic profile. The
CC polypeptides can be used to decrease or inhibit plasma leakage and/or
CC vascular permeability in a mammal.

SQ Sequence 38 BP; 9 A; 9 C; 11 G; 9 T; 0 other;

Query Match 50.7%; Score 15.2; DB 22; Length 38;
Best Local Similarity 71.4%; Pred. No. 2e+03;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 3 CATCCTGGGTAAGTGGACACCTGTG 30

DB 29 CTTCTGGGACACAGCTGATATCTATG 2

RESULT 9
AAA28244/C
ID AAA28244 standard; DNA; 45 BP.

AC AAA28244;

DT 12-FEB-2001 (first entry)

DE Upstream45 primer used in the construction of mutant YJR012C gene.

KW Essential gene identification; antifungal agent; yeast; germination;
KW growth; pseudohyphal growth; hyphal growth; proliferation; insecticide;
KW herbicide; PCR primer; YJR012C; ss.

OS Saccharomyces cerevisiae.

PN WO200058457-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08641.

PR 31-MAR-1999; 99US-0127272.

PA (ROSE-) ROSETTA INPHARMATICS INC.

PI Dimster-Denk DF;

DR WPI; 2000-594641/56.

PT Identifying a target gene for design or discovery of an antifungal
PT agent, insecticide, or herbicide, comprising disrupting the function of
PT a gene in a yeast cell and identifying whether the function is
PT essential for e.g. germination -

XX Example 3; Fig 15; 156pp; English.

CC This invention relates to a method for the identification of a target
CC gene useful for the design or discovery of an antifungal agent. The
CC method comprises disrupting the function of a gene in a yeast cell, and
CC identifying whether the function is essential for germination, growth,
CC pseudohyphal growth or hyphal growth. The invention further comprises
CC determining whether the protein encoded by the essential gene has
CC homology to a mammalian, plant or insect protein. The methods are useful
CC for identifying genes in Saccharomyces cerevisiae which are essential for
CC germination and proliferation of S. cerevisiae and using the identified
CC genes or their encoded proteins as targets for highly specific antifungal
CC agents, insecticides, herbicides and antiproliferation drugs. The
CC invention includes examples of the use of the method, comprising the
CC formation and characterisation of a number of S. cerevisiae genes to
CC determine if they are essential for growth of the yeast. The present
CC sequence represents a PCR primer used in the construction and analysis of
CC the S. cerevisiae YJR012C mutant strain.

SQ Sequence 45 BP; 20 A; 10 C; 7 G; 8 T; 0 other;

Query Match 50.7%; Score 15.2; DB 21; Length 45;
Best Local Similarity 85.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CATCCTGGGTAAGTGGGA 22
DB 45 CATCTTGGTAAGTGGCA 26

RESULT 10
ABL92859
ID ABL92859 standard; DNA; 22 BP.

AC ABL92859;
 XX
 DT 06-JUN-2002 (first entry)
 XX
 DE G protein-coupled receptor GPCR10 PCR primer SEQ ID NO:341.
 XX
 KW Human; G protein-coupled receptor; antidiabetic; anorectic; cytostatic;
 KW Immunomodulator; neuroprotective; nootropic; antiparkinsonian; metabolic;
 KW immunosuppressive; ophthalmological; antibacterial; vitrucoe; fungicide;
 KW protozoacide; hypertensive; hypotensive; analgesic; osteopathic;
 KW antitumor; antilasthmatic; antiallergic; anti-HIV; antileptic; vaccine;
 KW antifertility; antiinflammatory; haemostatic; cell signal processing;
 KW cardiomyopathy; atherosclerosis; metabolic pathway modulation; cancer;
 KW gene therapy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200212343-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 07-AUG-2001; 2001WO-US24787.
 XX
 PR 07-AUG-2000; 2000US-223138P.
 PR 07-AUG-2000; 2000US-223472P.
 PR 11-AUG-2000; 2000US-224613P.
 PR 11-AUG-2000; 2000US-224815P.
 PR 05-JAN-2001; 2001US-2600032P.
 PR 05-JAN-2001; 2001US-260072P.
 PR 08-JAN-2001; 2001US-260283P.
 PR 09-JAN-2001; 2001US-260450P.
 PR 10-JAN-2001; 2001US-261156P.
 PR 22-JAN-2001; 2001US-263338P.
 PR 23-JAN-2001; 2001US-263434P.
 PR 01-FEB-2001; 2001US-265704P.
 PR 20-FEB-2001; 2001US-269964P.
 PR 09-MAR-2001; 2001US-274873P.
 PR 15-MAR-2001; 2001US-276406P.
 PR 01-MAY-2001; 2001US-287916P.
 XX
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Spytek KA, Padigaru M, Zernhusen BD, Baumgartner JC, Li L;
 PI Casman SJ, Vernet CAM, Ballinger RA, Shenoy SG, Kekuda R;
 PI Burgess CE, Mezes PS, Grosse WM, Alsobrook JP, Gorman L;
 PI Larochele WJ, Taupier RJ, Colman SD, Szekeres ES;
 PI
 XX
 DR WPI: 2002-217180/27.
 XX
 PT New G-protein coupled receptor polypeptides and nucleic acids, useful
 PT for diagnosis, prevention or treatment of hematopoietic,
 PT neurodegenerative, immune and signal transduction pathway disorders -
 XX
 XX
 PS Example 2; Page 357; 492pp; English.
 XX
 CC The present invention describes novel human G protein-coupled receptors
 CC (GPCR) designated GPCR1-36 from the present invention. The GPCRs can have
 CC activities such as: antidiabetic; anorectic; immunomodulator; cytostatic;
 CC neuroprotective; nootropic; antiparkinsonian; analgesic; osteopathic;
 CC immunosuppressive; metabolic; ophthalmological; antibacterial; vitrucoe;
 CC fungicide; protozoacide; hypertensive; hypotensive; anti-HIV; antitumor;
 CC antilasthmatic; antileptic; antiallergic; antiinflammatory; haemostatic;
 CC and antiinflammatory. They can be used in gene therapy and vaccine
 CC production. The GPCR proteins can be used for treating or preventing
 CC GPCR-associated disorders such as cardiomyopathy, atherosclerosis, or a
 CC disorder related to cell signal processing and metabolic pathway
 CC modulation. In humans, GPCR proteins and the polynucleotides encoding
 CC them are useful for determining the presence of or predisposition to a
 CC disease, especially cancer associated with altered levels of GPCR
 CC proteins and polynucleotides, by measuring the level of protein
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. GPCR
 CC proteins are also useful for identifying an agent, especially cellular

CC receptor or a downstream effector that binds to GPCR, for screening of a
 CC candidate substance interacting with an olfactory receptor polypeptide,
 CC its fragments or variants. The present sequence represents a PCR primer
 CC used in the isolation of a novel human GPCR in the present invention.
 XX
 XX
 SO Sequence 22 BP; 7 A; 5 C; 6 G; 4 T; 0 other;

Query Match 49.3%; Score 14.8; DB 24; Length 22;
 Best local Similarity 88.9%; Pred. No. 2.8e+03;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 CATCTGGGTAAAGACGTGC 20
 |||||
 DB 5 CATCTGGGTAAAGACGTGC 22

RESULT 11
 AAA91083
 ID AAA91083 standard; DNA; 38 BP.
 XX
 AC AAA91083;
 XX
 DT 05-APR-2001 (first entry)
 XX
 DE PCR primer F11D2.VEGFR3D3.as for F11 receptor fusion DNA sequence.
 XX
 KW F11 receptor; fusion protein; chimeric protein; pharmacokinetic;
 KW plasma leakage; vascular permeability; IgG Fc region; PCR primer; ss.
 XX
 OS unidentified.
 XX
 PN WO200075319-A1.
 XX
 PD 14-DEC-2000.
 XX
 PR 23-MAY-2000; 2000WO-US14142.
 XX
 PR 08-JUN-1999; 99US-0138133.
 XX
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PI Papadopoulos NJ, Davis S, Yancopoulos GD;
 PI
 XX
 DR WPI: 2001-071076/08.
 XX
 PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,
 PT and its fragments, useful for diagnosis, evaluation, and treatment of
 PT diseases associated with the gene expression and for producing model
 PT systems -
 XX
 XX
 PS Example 17; Page 62; 159pp; English.
 XX
 CC This sequence represents a PCR primer used to construct DNA
 CC sequences encoding the fusion proteins of the invention between
 CC the F11 receptor and the Fc region of IgG. The specification relates
 CC to modified chimeric polypeptides with improved pharmacokinetics. The
 CC modified chimeric polypeptides are preferably F11 receptor polypeptides
 CC that have been modified to improve their pharmacokinetic profile. The
 CC polypeptides can be used to decrease or inhibit plasma leakage and/or
 CC vascular permeability in a mammal.
 XX
 SO Sequence 38 BP; 8 A; 6 C; 10 G; 14 T; 0 other;

Query Match 49.3%; Score 14.8; DB 22; Length 38;
 Best local Similarity 73.1%; Pred. No. 3e+03; 7; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 5 TCCTGGTAAAGACGTGCACCTGTG 30
 |||||
 DB 2 TCCTGGGACACGTGATATCTATG 27

RESULT 12

AA08201/c
ID AA08201 standard; DNA: 39 BP.
XX
AC AA08201:
XX
DT 28-MAY-1996 (first entry)
XX
DE Amplification primer BK138.
XX
KW Linker: interleukin-4; interleukin-2; IL-4; IL-2; G-CSF; GM-CSF;
KW granulocyte-colony stimulating factor; circularly permuted ligand;
KW cancer; therapy; granulocyte macrophage-colony stimulating factor;
KW polymerase chain reaction; PCR; primer; amplify; ss.
XX
OS Synthetic.
XX
PN WO9527732-A2.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US04468.
XX
PR 08-APR-1994; 94US-0225224.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kreltman RJ, Pastan I;
XX
DR WPI: 1995-366354/47.
XX
PT Circularly permuted ligands and chimeric mols. are modified
PT interleukin(s) or colony-stimulating factors - with increased
PT binding specificity and affinity for inhibiting tumours
XX
PS Example 5; Page 35; 97pp; English.
XX
CC AA08176-T08219 represent amplification primers used in the construction
CC of modified ligands. The modified ligands comprise two copies of a
CC sequence joined to a linker. The sequences used in the ligand include
CC interleukin-4 (IL-4), IL-2, granulocyte-colony stimulating factor
CC (G-CSF) and granulocyte macrophage-colony stimulating factor (GM-CSF).
CC The linker regions used are represented by AAR87726 and AAR87730. This
CC sequence was used in conjunction with AA08200 to amplify codons 39-127
CC of IL-2 for use in a modified ligand. These modified ligands are known
CC as circularly permuted ligands. The modified ligands can be joined to
CC another protein (preferably a cytotoxin or an antibody) using a spacer
CC (see AAR87732-R87734). The circularly permuted ligands have greater
CC specificity and binding affinity than the original ligand. They can be
CC used in chimeric molecules to inhibit the growth of tumour cells in vivo,
CC where the two copies of the protein sequence are joined to cytotoxins.
XX
SO Sequence 39 BP; 7 A; 10 C; 12 G; 10 T; 0 other;
Query Match 49.3%; Score 14.8; DB 16; Length 39;
Best Local Similarity 73.1%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 2 TCATCTGGGTAAAGTGGGACACT 27
DB 26 TCACCGAGGTAAACGGTGGGACACT 1

RESULT 13
AA08198
ID AA08198 standard; DNA: 42 BP.
XX
AC AA08198:
XX
DT 28-MAY-1996 (first entry)
XX
DE Amplification primer BK135.
XX
KW Linker: interleukin-4; interleukin-2; IL-4; IL-2; G-CSF; GM-CSF;

KW granulocyte-colony stimulating factor; circularly permuted ligand;
KW cancer; therapy; granulocyte macrophage-colony stimulating factor;
KW polymerase chain reaction; PCR; primer; amplify; ss.
XX
OS Synthetic.
XX
PN WO9527732-A2.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1995; 95WO-US04468.
XX
PR 08-APR-1994; 94US-0225224.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kreltman RJ, Pastan I;
XX
DR WPI: 1995-366354/47.
XX
PT Circularly permuted ligands and chimeric mols. are modified
PT interleukin(s) or colony-stimulating factors - with increased
PT binding specificity and affinity for inhibiting tumours
XX
PS Example 5; Page 35; 97pp; English.
XX
CC AA08176-T08219 represent amplification primers used in the construction
CC of modified ligands. The modified ligands comprise two copies of a
CC sequence joined to a linker. The sequences used in the ligand include
CC interleukin-4 (IL-4), IL-2, granulocyte-colony stimulating factor
CC (G-CSF) and granulocyte macrophage-colony stimulating factor (GM-CSF).
CC The linker regions used are represented by AAR87726 and AAR87730. This
CC sequence was used in conjunction with AA08199 to amplify a codons 1-38
CC of IL-2 for use in a modified ligand. These modified ligands are known
CC as circularly permuted ligands. The modified ligands can be joined to
CC another protein (preferably a cytotoxin or an antibody) using a spacer
CC (see AAR87732-R87734). The circularly permuted ligands have greater
CC specificity and binding affinity than the original ligand. They can be
CC used in chimeric molecules to inhibit the growth of tumour cells in vivo,
CC where the two copies of the protein sequence are joined to cytotoxins;
XX
SO Sequence 42 BP; 10 A; 12 C; 11 G; 9 T; 0 other;
Query Match 49.3%; Score 14.8; DB 16; Length 42;
Best Local Similarity 73.1%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 2 TCATCTGGGTAAAGTGGGACACT 27
DB 5 TCACCGAGGTAAACGGTGGGACACT 30

RESULT 14
AAH76860/c
ID AAH76860 standard; DNA: 24 BP.
XX
AC AAH76860:
XX
DT 14-DEC-2001 (first entry)
XX
DE Human tyrosinase 15 RT-PCR primer, SEQ ID NO:4.
XX
KW Human: tyrosinase 15; recombinant production;
KW malignant tumour; cancer; blood disease; HIV infection;
KW human immunodeficiency virus; immune disorder; inflammatory condition;
KW cytostatic; anti-HIV; antiinflammatory; immunomodulator;
KW reverse transcription-PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200171001-A1.
XX
PD 27-SEP-2001.

```
XX 19-MAR-2001; 2001WO-CN00357.
PF
XX
XX 22-MAR-2000; 2000CN-0115044.
PR
XX
XX (BIOW-) BIOWINDOM GENE DEV INC SHANGHAI.
PA
XX
XX Mao Y, Xie Y;
PI
XX
XX WPI; 2001-602790/68.
DR
XX
XX Human tyrosinase 15 and encoded polynucleotide, used in diagnosis and
PT treatment of malignant tumors, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and inflammation -
XX
XX
XX Example 2; Page 11; 33pp; Chinese.
PS
XX
XX The invention relates to human tyrosinase 15 (AA66766), nucleic acids
CC encoding it (AAH76858), and a method for the recombinant production of
CC tyrosinase 15. The protein has a molecular weight of 15 kD. The present
CC invention additionally discloses an antagonist of tyrosinase 15 for
CC therapeutic use, and an antibody which specifically binds to tyrosinase
CC 15. Tyrosinase 15, and nucleotides which encode it may be used for
CC treating a variety of diseases, such as malignant tumors, blood
CC diseases, HIV (human immunodeficiency virus) infection, immune disorders
CC and inflammatory conditions. The protein may also be used to screen for
CC modulators of its activity or for peptide fingerprinting identification.
CC The polynucleotide can be used as a primer for nucleic acid amplification
CC reactions or as a probe for hybridisation reactions, or in producing gene
CC chips or microarrays. Sequences AAH76859-AAH76860 represent reverse
CC transcription-PCR (RT-PCR) primers used in an exemplification of the
CC invention to isolate human tyrosinase 15 cDNA.
XX
XX Sequence 24 BP; 3 A; 9 C; 8 G; 4 T; 0 other;
SQ
XX
XX Query Match 48.7%; Score 14.6; DB 22; Length 24;
XX Best Local Similarity 81.0%; Pred. No. 3.5e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 CCTGGGTAGAGTGGGACCC 26
XX ||||| ||||| |||||
DB 23 CCTGGGTAGAGTGGGACCC 3
XX
XX RESULT 15
XX AAA88764
XX ID AAA88764 standard; DNA; 33 BP.
XX
XX AAA88764;
AC
XX
XX 19-FEB-2001 (first entry)
XX
XX Respiratory syncytial virus NS1-NS2 gene fusion region.
DE
XX
XX RSV; vaccine; attenuation; pneumonia; bronchiolitis; NS1 gene;
KM NS2 gene; mutant; ss.
XX
XX Human respiratory syncytial virus.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX FT 5'UTR 1..23
XX FT /*tag= a
XX FT /note= "NS1 nontranslated region"
XX CDS 24..35
XX FT /*tag= b
XX FT /partial
XX FT /note= "5' end of NS2 open reading frame"
XX
XX WO200061611-A2.
XX
XX 19-OCT-2000.
XX
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```
PF 31-MAR-2000; 2000WO-US08802.
XX
XX 13-APR-1999; 99US-0291894.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Collins PL, Murphy BR, Whitehead SS;
PI
XX
XX WPI; 2000-679462/66.
DR
XX
XX Infectious chimeric respiratory syncytial virus (RSV) produced from
PT cloned nucleotide sequences, useful as a vaccine against diseases
PT caused by the virus, such as pneumonia and bronchiolitis -
XX
XX
XX Example 17; Fig 21; 280pp; English.
PS
XX
XX The present sequence represents a fusion of human respiratory
CC syncytial virus (RSV) NS1 gene 5' nontranslated region to the
CC NS2 coding region. PCR-mediated mutagenesis (see AAA88760-61) was
CC used to delete the NS1 gene coding region, 3' untranslated region,
CC the NS1-NS2 coding region and the NS2 5' nontranslated region, a
CC total of 529 nucleotides. The deleted region corresponds to
CC nucleotides 99-627 of the RSV antigenome cDNA given in AAA88743.
CC This type of deletion can be incorporated into viable recombinant
CC RSV of the invention to yield an altered phenotype, in this case
CC reduced rate of virus growth and reduced plaque size in vitro. The
CC invention relates to infectious chimeric RSV produced by introducing
CC 1 or more heterologous gene(s) or gene segment(s) from 1 RSV
CC subgroup or strain into a recipient RSV background of a different
CC subgroup or strain. The resulting chimeric RSV virus or subviral
CC particle is infectious and attenuated, preferably by introduction
CC of selected mutations. The chimeric RSV is useful as a vaccine
CC against RSV, which causes pneumonia and bronchiolitis in infants.
XX
XX Sequence 33 BP; 12 A; 7 C; 6 G; 8 T; 0 other;
SQ
XX
XX Query Match 48.7%; Score 14.6; DB 21; Length 33;
XX Best Local Similarity 81.0%; Pred. No. 3.7e+03;
XX Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 TCCTGGGTAGAGTGGGACAC 25
XX ||||| ||||| |||||
DB 9 TCCTGGGTAGAGTGGGACAC 29
XX
```

Search completed: June 21, 2003, 22:26:18
Job time : 167.531 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 21:30:22 ; Search time 35.625 Seconds
(without alignments)
258.254 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCACTCTGGTAAAGAGTGGACACCTGTG 30

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 443362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/1/lna/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/lna/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	52.7	31	2	US-08-454-557C-63 Sequence 63, Appl
2	15.8	52.7	31	2	US-08-340-426D-63 Sequence 63, Appl
3	15.8	52.7	31	2	US-08-450-673C-63 Sequence 63, Appl
4	15.8	52.7	31	5	PCT-US95-1711A-63 Sequence 63, Appl
5	14.8	49.3	39	1	US-08-225-224-31 Sequence 31, Appl
6	14.8	49.3	39	3	US-08-225-224-31 Sequence 31, Appl
7	14.8	49.3	39	5	PCT-US95-04468-31 Sequence 31, Appl
8	14.8	49.3	42	1	US-08-225-224-28 Sequence 28, Appl
9	14.8	49.3	42	3	US-08-722-258-28 Sequence 28, Appl
10	14.8	49.3	42	5	PCT-US95-04468-28 Sequence 28, Appl
11	14.6	48.7	45	5	US-08-931-220-38 Sequence 38, Appl
12	14.6	48.7	45	5	PCT-US95-11723-38 Sequence 38, Appl
13	14.6	48.7	45	5	PCT-US96-05997-38 Sequence 38, Appl
14	14.2	47.3	20	4	US-09-742-703-12 Sequence 12, Appl
15	14.2	47.3	42	4	US-09-171-425-2 Sequence 2, Appl
16	14.2	47.3	48	4	US-09-171-425-6 Sequence 6, Appl
17	14.2	47.3	48	4	US-09-171-425-7 Sequence 7, Appl
18	14.2	47.3	46	1	US-07-977-434-38 Sequence 38, Appl
19	14.2	46.7	46	1	US-08-458-819-38 Sequence 38, Appl
20	14.2	46.7	46	3	PCT-US91-07035-38 Sequence 38, Appl
21	14.2	46.7	46	4	US-09-641-638-659 Sequence 659, App
22	13.8	46.0	26	4	US-08-859-998-1306 Sequence 1306, App
23	13.8	46.0	26	3	US-09-225-928-1306 Sequence 1306, App
24	13.8	46.0	36	3	US-09-041-953-5 Sequence 5, Appl
25	13.8	46.0	43	2	US-08-332-766A-5 Sequence 54, Appl
26	13.4	44.7	40	2	US-08-628-422-54 Sequence 60, Appl
27	13.4	44.7	40	4	US-09-306-998-60

28	13.4	44.7	50	1	US-08-171-389-326 Sequence 326, App
29	13.4	44.7	50	1	US-08-123-936-326 Sequence 326, App
30	13.4	44.7	50	2	US-08-475-228A-326 Sequence 326, App
31	13.4	44.7	50	3	US-08-482-080A-326 Sequence 326, App
32	13.4	44.7	50	4	US-09-354-947-326 Sequence 326, App
33	13.4	44.7	50	5	PCT-US93-12388-326 Sequence 326, App
34	13.2	44.0	20	3	US-08-882-046-61 Sequence 61, Appl
35	13.2	44.0	26	1	US-08-621-914A-13 Sequence 13, Appl
36	13.2	44.0	33	1	US-08-244-626-30 Sequence 30, Appl
37	13.2	44.0	35	6	5256642-27 Patent No. 5256642
38	13.2	44.0	35	6	5472939-27 Patent No. 5472939
39	13.2	44.0	38	4	US-08-870-511-34 Sequence 34, Appl
40	13.2	44.0	39	1	US-08-469-486-33 Sequence 33, Appl
41	13.2	44.0	39	2	US-08-469-658-33 Sequence 33, Appl
42	13.2	44.0	42	6	5256642-28 Patent No. 5256642
43	13.2	44.0	42	6	5472938-28 Patent No. 5472938
44	13	43.3	24	5	PCT-US96-10905-23 Sequence 23, Appl
45	13	43.3	28	2	US-08-761-243C-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-454-557C-63/C
; Sequence 63, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Mandis, Jack R.
; TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ. ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-454-557C-63
Query Match 52.7%; Score 15.8; DB 2; Length 31;
Best Local Similarity 74.1%; Pred. No. 93;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 1 TTCACTCTGGTAAAGAGTGGACACT 27
DB 27 TTCACTCTGGTAAAGAGTGGACACT 1

QY 1 TTCATCCTGGTGAAGAGTGGGACACCT 27
||||| ||||| ||||| ||||| |||||
Db 27 TTCAGCCTGGGTGACGACGACGACATCT 1

RESULT 5

US-08-225-224-31/c
Sequence 31, Application US/08225224
Patent No. 5635599

GENERAL INFORMATION:

APPLICANT: PASTAN, Ira
APPLICANT: KREITMAN, Robert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (primer)
US-08-225-224-31

Query Match 49.3%; Score 14.8; DB 1; Length 39;
Best Local Similarity 73.1%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGTGAAGAGTGGGACACCT 27
||||| ||||| ||||| ||||| |||||
Db 26 TCACCGAGGTAACTGGGCGACCT 1

RESULT 6

US-08-722-258-31/c
Sequence 31, Application US/08722258
Patent No. 6011002

GENERAL INFORMATION:

APPLICANT: Pastan, Ira
APPLICANT: Kreitman, Robert J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED CHIMERIC MOLECULES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY:
LOCATION: 1..39
OTHER INFORMATION: /note= "BK-138 primer"
US-08-722-258-31

Query Match 49.3%; Score 14.8; DB 3; Length 39;
Best Local Similarity 73.1%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGTGAAGAGTGGGACACCT 27
||||| ||||| ||||| ||||| |||||
Db 26 TCACCGAGGTAACTGGGCGACCT 1

RESULT 7
PCT-US95-04468-31/c
Sequence 31, Application PC/TUS9504468
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
NUMBER OF SEQUENCES: 59
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468
FILING DATE: 07-APR-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-193-1PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
PCT-US95-04468-31

Query Match 49.3%; Score 14.8; DB 5; Length 39;
Best Local Similarity 73.1%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27
||| | |||| | |||| | ||||
Db 26 TCACCGAGGTACGCGTGGGACACT 1

RESULT 8
US-08-225-224-28
Sequence 28, Application US/08225224
Patent No. 5635599

GENERAL INFORMATION:
APPLICANT: PASTAN, Ira
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 13280-193
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
US-08-225-224-28

Query Match 49.3%; Score 14.8; DB 1; Length 42;
Best Local Similarity 73.1%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27
||| | |||| | |||| | ||||
Db 5 TCACCGAGGTACGCGTGGGACACT 30

RESULT 9
US-03-722-258-28
Sequence 28, Application US/08722258
Patent No. 6011002

GENERAL INFORMATION:
APPLICANT: Pastan, Ira
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION MOLECULES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,258
FILING DATE: 08-JAN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/04468
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/225,224
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION/DOCKET NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-193100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..42
OTHER INFORMATION: /note= "BK-135 primer"

US-08-722-258-28

Query Match 49.3%; Score 14.8; DB 3; Length 42;
Best Local Similarity 73.1%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TCATCCTGGGTAGAGTGGACACT 27
||| | |||| | |||| | ||||
Db 5 TCACCGAGGTACGCGTGGGACACT 30

RESULT 10
PCT-US95-04468-28
Sequence 28, Application PC/TUS9504468
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
NUMBER OF SEQUENCES: 59
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04468

FILING DATE: 07-APR-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/225,224
 FILING DATE: 08-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen L.
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 15280-193-1PC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (primer)
 PCT-US95-04468-28

Query Match 49.3% Score 14.8; DB 5; Length 42;
 Best Local Similarity 73.1%; Pred. No. 2.9e+02;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 2 TCATCTGGGTAAGAGTGGACACCT 27
 ||| ||| ||| ||| ||| ||| |||
 Db 5 TCACCGAGGTAACGGTGGGACACCT 30

RESULT 11
 US-08-931-220-38/c
 Sequence 38, Application US/08931220
 Patent No. 6030835
 GENERAL INFORMATION:
 APPLICANT: Musser M.D., James M.
 APPLICANT: Kapur M.D., Vivek
 TITLE OF INVENTION: Methods and Compositions for Identifying
 TITLE OF INVENTION: Group A Streptococcus
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WEIL, GOTSHAL & MANCES
 STREET: 2882 Sand Hill Road, Suite 280
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025-7022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/931,220
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,542
 FILING DATE: 14-SEP-1994
 APPLICATION NUMBER: US 08/160,965
 FILING DATE: 02-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Rae-Venter Ph.D., Barbara
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: BAYL-004/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 926-6200
 TELEFAX: (415) 854-3713
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pyogenes
 IMMEDIATE SOURCE:
 CLONE: speb19
 US-08-931-220-38

Query Match 48.7% Score 14.6; DB 3; Length 45;
 Best Local Similarity 69.0%; Pred. No. 3.7e+02;
 Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 2 TCATCTGGGTAAGAGTGGACACCTG 30
 ||| ||| ||| ||| ||| ||| |||
 Db 33 TCATCTGGGTAAGAGTGGACACTTTG 5

RESULT 12
 PCT-US95-11723-38/c
 Sequence 38, Application PC/TUS9511723
 GENERAL INFORMATION:
 APPLICANT: Musser M.D., James M.
 APPLICANT: Kapur M.D., Vivek
 TITLE OF INVENTION: Methods and Compositions for
 TITLE OF INVENTION: Identifying Streptococcus
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAW OFFICES OF BARBARA RAE-VENTER
 STREET: P.O. Box 60039
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/11723
 FILING DATE: 14-SEP-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/306,542
 FILING DATE: 14-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Rae-Venter Ph.D., Barbara
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: BAYL-004/03US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 926-6205
 TELEFAX: (415) 424-8760
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Streptococcus pyogenes
 IMMEDIATE SOURCE:
 CLONE: speb19
 PCT-US95-11723-38

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 30
||||| ||||| ||||| |||||
Db 33 TCATGTTGGGAAGGCGGACACTTTG 5

RESULT 13

PCT-US96-05997-38/c
Sequence 38, Application PC/TUS9605997
GENERAL INFORMATION:
APPLICANT: Musser M.D., James M.
APPLICANT: Kapur M.D., Vivek
APPLICANT: Ananthaswamy, H. N.
APPLICANT: Fernandez, A.
TITLE OF INVENTION: Use of extracellular cysteine protease
TITLE OF INVENTION: to inhibit cell proliferation
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEIL, GOTSAL & MANGES
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025-7022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05997
FILING DATE: 01-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,542
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,965
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter Ph.D., Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: BAYL-004/0205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pyogenes
IMMEDIATE SOURCE:
CLONE: speB19
PCT-US96-05997-38

Query Match 48.7%; Score 14.6; DB 5; Length 45;
Best Local Similarity 69.0%; Pred. No. 3.7e+02;
Matches 20; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 30
||||| ||||| ||||| |||||
Db 33 TCATGTTGGGAAGGCGGACACTTTG 5

RESULT 14
US-09-742-703-12
Sequence 12, Application US/09742703
Patent No. 6423543

GENERAL INFORMATION:
APPLICANT: Patrick Allen Marcotte
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF HEP5IN EXPRESSION
FILE REFERENCE: RTS-0090
CURRENT APPLICATION NUMBER: US/09/742,703
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 12
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-742-703-12

Query Match 47.3%; Score 14.2; DB 4; Length 20;
Best Local Similarity 84.2%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 TCCTGGGTAAGAGTGGGAC 23
||||| ||||| ||||| |||||
Db 2 TCCTGGGCAAGGAGTGGAC 20

RESULT 15

US-09-171-425-2
Sequence 2, Application US/09171425A
Patent No. 6465438
GENERAL INFORMATION:
APPLICANT: Schorf, Joachim
APPLICANT: Baker, Henry J.
APPLICANT: Smith, Bruce F.
TITLE OF INVENTION: NUCLEIC ACID VACCINATION FOR PARVOVIRAL INFECTIONS
FILE REFERENCE: 08909/003001
CURRENT APPLICATION NUMBER: US/09/171,425A
CURRENT FILING DATE: 1998-10-19
EARLIER APPLICATION NUMBER: PCT/EP97/01943
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 42
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated oligonucleotides
US-09-171-425-2

Query Match 47.3%; Score 14.2; DB 4; Length 42;
Best Local Similarity 70.4%; Pred. No. 5.6e+02;
Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 2 TCATCCTGGGTAAGAGTGGGACACTGTG 28
||||| ||||| ||||| |||||
Db 14 TCACCTGGGCTAAGAAAGAAAGACTG 40

Search completed: June 22, 2003, 00:01:29
Job time : 38.625 secs

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 22:26:37 ; Search time 88.5938 seconds
(without alignments)
496.907 Million cell updates/sec

Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCATCTCGGTAGAGTGGACACCTGTG 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	9	US-09-964-667-9
2	30	100.0	30	9	US-09-964-666-9
3	30	100.0	30	10	US-09-964-412-9
4	22	73.3	22	9	US-09-964-667-5
5	22	73.3	22	10	US-09-964-666-5
6	22	73.3	22	10	US-09-964-412-5
7	15.6	52.0	25	9	US-10-098-263B-65996
8	15.2	50.7	45	10	US-09-965-602-27
9	15	50.0	43	9	US-09-802-640-9
10	14.8	49.3	30	9	US-10-085-906-97
11	14.8	49.3	31	10	US-09-801-274-8
12	14.6	48.7	25	9	US-10-215-112-7585
13	14.6	48.7	25	9	US-10-215-112-12152
14	14.6	48.7	25	9	US-10-098-263B-97774
15	14.6	48.7	25	9	US-10-098-263B-129375
16	14.4	48.0	49	9	US-09-860-670-233
17	14.2	47.3	25	9	US-10-098-263B-3274
18	14.2	47.3	36	9	US-10-294-778-8
19	14.2	47.3	39	9	US-10-011-672-9

20	14.2	47.3	39	9	US-10-012-013-9	Sequence 9, Appl
21	14.2	47.3	39	9	US-10-012-070A-9	Sequence 9, Appl
22	14	46.7	25	9	US-10-098-263B-44679	Sequence 44679, A
23	14	46.7	25	9	US-10-098-263B-65995	Sequence 65995, A
24	14	46.7	31	9	US-09-912-263-86	Sequence 86, Appl
25	13.8	46.0	31	10	US-09-801-274-873	Sequence 873, App
26	13.6	45.3	25	9	US-10-060-895A-1142	Sequence 1142, Ap
27	13.6	45.3	25	9	US-10-060-895A-1143	Sequence 1143, Ap
28	13.6	45.3	25	9	US-10-060-895A-1144	Sequence 1144, Ap
29	13.6	45.3	25	9	US-10-060-895A-1145	Sequence 1145, Ap
30	13.6	45.3	25	9	US-10-060-895A-1146	Sequence 1146, Ap
31	13.6	45.3	25	9	US-10-060-895A-1147	Sequence 1147, Ap
32	13.6	45.3	25	9	US-10-060-895A-1148	Sequence 1148, A
33	13.6	45.3	25	9	US-10-098-263B-103720	Sequence 103720,
34	13.4	44.7	25	9	US-10-098-263B-26559	Sequence 26559, A
35	13.4	44.7	25	9	US-10-098-263B-26737	Sequence 26737, A
36	13.4	44.7	25	9	US-10-098-263B-103293	Sequence 103293,
37	13.4	44.7	25	9	US-10-098-263B-125737	Sequence 125737,
38	13.4	44.7	30	9	US-10-082-772-9	Sequence 9, Appl
39	13.4	44.7	31	9	US-09-864-636A-2477	Sequence 2477, Ap
40	13.4	44.7	40	9	US-09-951-402-60	Sequence 60, Appl
41	13.4	44.7	40	10	US-09-922-101-60	Sequence 60, Appl
42	13.4	44.7	25	9	US-10-060-895A-1148	Sequence 1148, Ap
43	13.2	44.0	25	9	US-10-060-895A-1149	Sequence 1149, Ap
44	13.2	44.0	25	9	US-10-098-263B-19558	Sequence 19558, A
45	13.2	44.0	25	9		

ALIGNMENTS

RESULT 1
US-09-964-667-9
Sequence 9, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Wands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-667-9

Query Match 100.0%; Score 30; DB 9; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

RESULT 2

US-09-964-666-9

Sequence 9, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-666-9

Query Match 100.0%; Score 30; DB 10; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

RESULT 3

US-09-964-412-9

Sequence 9, Application US/09964412

Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-964-412-9

Query Match 100.0%; Score 30; DB 10; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.00015;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

DB 1 TTTCATCTGGGTAAAGAGTGGGACACCTGTG 30

RESULT 4

US-09-964-667-5/C

Sequence 5, Application US/09964667

Publication No. US2003003621A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Preventio

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESSES:

ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,667

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.


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1      REGISTRATION NUMBER: 32,893
2      REFERENCE/DOCKET NUMBER: 0609.4370000
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: 202-371-2540
5      TELEFAX: 202-371-2540
6      INFORMATION FOR SEQ ID NO: 5:
7      SEQUENCE CHARACTERISTICS:
8      LENGTH: 22 base pairs
9      TYPE: nucleic acid
10     STRANDEDNESS: single
11     TOPOLOGY: linear
12     MOLECULE TYPE: cDNA
13     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
14     US-09-964-667-5
15
16     Query Match      73.3%; Score 22; DB 9; Length 22;
17     Best Local Similarity 100.0%; Pred. No. 0.74;
18     Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
19
20     3 CATCCTGGGTAGAGTGGGACA 24
21     ||||||||||||||||||||
22 CATCCTGGGTAGAGTGGGACA 1
23
24 RESULT 5
25 US-09-964-666-5/c
26 Sequence 5, Application US/09964666
27 Patent No. US20020104108A1
28 GENERAL INFORMATION:
29 APPLICANT: de la Monte, Suzanne
30 Mands, Jack R.
31 TITLE OF INVENTION: Transgenic Animals and Cell Lines for
32 Screening Drugs Effective for the Treatment or Prevention
33 of Alzheimer's Disease
34 NUMBER OF SEQUENCES: 14
35 CORRESPONDENCE ADDRESS:
36 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
37 STREET: 1100 New York Ave., Suite 600
38 CITY: Washington
39 STATE: DC
40 COUNTRY: USA
41 ZIP: 20005-3934
42 COMPUTER READABLE FORM:
43 MEDIUM TYPE: Floppy disk
44 COMPUTER: IBM PC compatible
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: PatentIn Release #1.0, Version #1.30
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/09/964,666
49 FILING DATE: 28-Sep-2001
50 CLASSIFICATION: <Unknown>
51 ATTORNEY/AGENT INFORMATION:
52 NAME: Esmond, Robert W.
53 REGISTRATION NUMBER: 32,893
54 REFERENCE/DOCKET NUMBER: 0609.4370000
55 TELECOMMUNICATION INFORMATION:
56 TELEPHONE: 202-371-2540
57 TELEFAX: 202-371-2540
58 INFORMATION FOR SEQ ID NO: 5:
59 SEQUENCE CHARACTERISTICS:
60 LENGTH: 22 base pairs
61 TYPE: nucleic acid
62 STRANDEDNESS: single
63 TOPOLOGY: linear
64 MOLECULE TYPE: cDNA
65 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
66 US-09-964-666-5
67
68     Query Match      73.3%; Score 22; DB 10; Length 22;
69     Best Local Similarity 100.0%; Pred. No. 0.74;
70     Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
71
72     3 CATCCTGGGTAGAGTGGGACA 24

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Db          22 CATCTGGGTAGAGTGGGACA 1
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RESULT 6
US-09-964-412-5/c
: Sequence 5, Application US/09964412
: Patent No. US20020129391A1
: GENERAL INFORMATION:
:   APPLICANT: de la Monte, Suzanne
:             Wands, Jack R.
: TITLE OF INVENTION: Transgenic Animals and Cell Lines for
:                   Screening Drugs Effective for the Treatment or Prevention
:                   of Alzheimer's Disease
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
:   STREET: 1100 New York Ave., Suite 600
:   CITY: Washington
:   STATE: DC
:   COUNTRY: USA
:   ZIP: 20005-3934
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/964,412
:   FILING DATE: 28-Sep-2001
:   CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
:   NAME: Esmond, Robert W.
:   REGISTRATION NUMBER: 32,893
:   REFERENCE/DOCKET NUMBER: 0609.4370000
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: 202-371-2540
:   TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 5:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 22 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:   MOLECULE TYPE: cDNA
:   SEQUENCE DESCRIPTION: SEQ ID NO: 5:
:
: US-09-964-412-5
:
: Query Match          73.3%, Score 22; DB 10; Length 22;
: Best Local Similarity 100.0%; Pred. No. 0.74;
: Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY          3 CATCTGGGTAGAGTGGGACA 24
:             |||||||
: Db          22 CATCTGGGTAGAGTGGGACA 1
:
: RESULT 7
: US-10-098-263B-65996
: Sequence 65996, Application US/10098263B
: Publication No. US2003010410A1
: GENERAL INFORMATION:
:   APPLICANT: Miltman, Michael
:   TITLE OF INVENTION: Human Microarray
:   FILE REFERENCE: 3118.1
:   CURRENT APPLICATION NUMBER: US/10/098,263B
:   CURRENT FILING DATE: 2003-01-08
:   PRIOR APPLICATION NUMBER: 60/276,759
:   PRIOR FILING DATE: 2001-03-16
:   NUMBER OF SEQ ID NOS: 131066
:   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
:   SEQ ID NO 65996
:   LENGTH: 25

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TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-65996

Query Match 52.0%; Score 15.6; DB 9; Length 25;
Best Local Similarity 81.8%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 TCCTGGGTAGAGTGGACACC 26
||| ||| ||| ||| ||| ||| |||
DB 3 TCCTGGGTAGAGTGGACACC 24

RESULT 8
US-09-965-602-27/c
Sequence 27, Application US/09965602
Patent No. US20020103154A1
GENERAL INFORMATION:
APPLICANT: Dimster-Deak, Dago
TITLE OF INVENTION: ESSENTIAL GENES IN YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS,
TITLE OF INVENTION: HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION DRUGS
FILE REFERENCE: ACA-8
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/965,602
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US/09/539,697
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 45
TYPE: DNA
ORGANISM: primer
US-09-965-602-27

Query Match 50.7%; Score 15.2; DB 10; Length 45;
Best Local Similarity 85.0%; Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 CATCTGGGTAGAGTGGGA 22
||| ||| ||| ||| ||| ||| |||
DB 45 CATCTGGGTAGAGTGGGA 26

RESULT 9
US-09-802-640-9/c
Sequence 9, Application US/09802640
Publication No. US20030036057A1
GENERAL INFORMATION:
APPLICANT: Braun, Andreas
APPLICANT: Bonsal Aruna
APPLICANT: Kleya Patrick
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
FILE REFERENCE: 24736-2048
CURRENT APPLICATION NUMBER: US/09/802,640
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 43
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
US-09-802-640-9

Query Match 50.0%; Score 15; DB 9; Length 43;
Best Local Similarity 78.3%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 8 TGGTAAGAGTGGACACCTGTG 30
| |||| | |||| |||| |||| ||||

DB 40 TAGTAGCGGTGGTACCCTGTG 18

RESULT 10
US-10-085-906-97
Sequence 97, Application US/10085906
Publication No. US20030054371A1
GENERAL INFORMATION:
APPLICANT: Ying, Vincent
APPLICANT: Wu, Paul
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
TITLE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF
FILE REFERENCE: GNN-5343CP2
CURRENT APPLICATION NUMBER: US/10/085,906
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 60/126,215
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 09/534,061
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: PCT/US00/07938
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 545
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-10-085-906-97

Query Match 49.3%; Score 14.8; DB 9; Length 30;
Best Local Similarity 73.1%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCTGGGTAGAGTGGACACC 26
| |||| |||| | || | ||| |||
DB 1 TCATCTGGGTGGGACAGAGACTCC 26

RESULT 11
US-09-801-274-8
Sequence 8, Application US/09801274
Patent No. US20020032319A1
GENERAL INFORMATION:
APPLICANT: Carilli, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2009-001
CURRENT APPLICATION NUMBER: US/09/801,274
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/187,510
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/206,129
PRIOR FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 1802
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-274-8

Query Match 49.3%; Score 14.8; DB 10; Length 31;
Best Local Similarity 67.9%; Pred. No. 1.6e+03;
Matches 19; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 3 CATCTGGGTAGAGTGGACACCTGTG 30
||| ||| | : || |||| |||| |
DB 2 CATCAAGGATGATGATGACACTGCG 29

RESULT 12

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US-10-215-112-7585
; Sequence 7585, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7585:
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-7585

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTGGTAAGAGTGGGACACCT 27
Db 2 CTAGGAAGGTTGGGACACCT 22

RESULT 13
US-10-215-112-12152/c
; Sequence 12152, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12152
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12152

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 CTGGTAAGAGTGGGACACCT 27
Db 24 CTAGGAAGGTTGGGACACCT 4

RESULT 14
US-10-098-263B-97774/c
; Sequence 97774, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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```
; SEQ ID NO 97774
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-97774

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 TGGGTAAGAGTGGGACACCTG 28
Db 23 TGTGTAAGAGTGGTACCACCTG 3

RESULT 15
US-10-098-263B-129375/c
; Sequence 129375, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 129375
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-129375

Query Match
Best Local Similarity 48.7%; Score 14.6; DB 9; Length 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 TCCTGGGTAAGAGTGGGACAC 25
Db 25 TCCTGGGTCGAGTGTCCACAC 5
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OM nucleic - nucleic search, using sw model

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Title: US-09-964-666-9

Perfect score: 30

Sequence: 1 TTCATCTGCTGAGAGTGGACACCTGTG 30

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estrpl:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_hic3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_hum:*
20: em_gss_hum:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mam:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	16.6	55.3	48	14	H39590	YP01907.r1
2	16.4	54.7	50	9	AU102898	AU102898
3	16.4	54.7	50	9	AU106860	AU106860
4	16.2	54.0	48	17	A2796512	A2796512 2M0052H18
5	16	53.3	50	9	AU106864	AU106864
6	15.4	51.3	46	9	AI439612	AI439612 tc91b01.x

Result No.	Score	Match	Length	DB	ID	Description
7	15.4	51.3	50	9	AI024893	AI024893 ou52b04.x
8	15	50.0	47	14	R08290	R08290 yf18e09.s1
9	14.8	49.3	35	14	N38850	N38850 yf80e11.f1
10	14.8	49.3	40	17	A2575761	A2575761 AST--732B0
11	14.8	49.3	48	9	AU258691	AU258691 AU258691
12	14.8	49.3	50	9	AU108052	AU108052 AU108052
13	14.6	48.7	46	9	AI900587	AI900587 sc13c051.y
14	14.6	48.7	46	9	AA871520	AA871520 yq36e07.f1
15	14.4	48.0	42	14	H99413	H99413 yx24f02.s1
16	14.4	48.0	42	14	T96362	T96362 yx49c04.s1
17	14.4	48.0	50	9	AU104029	AU104029 AU104029
18	14.4	48.0	50	9	AU107906	AU107906 AU107906
19	14.2	47.3	35	10	AV951566	AV951566 AV951566
20	14.2	47.3	45	17	DR1384T	DR1384T Danio fer
21	14.2	47.3	49	9	AI697225	AI697225 tg17d081.x
22	14.2	47.3	50	9	AU103750	AU103750 AU103750
23	14.2	47.3	37	13	BI522018	BI522018 603081709
24	14	46.7	49	14	D11989	D11989 HUM0005134
25	13.8	46.0	30	14	H39150	H39150 ym83e09.f1
26	13.8	46.0	39	14	H84235	H84235 ym65f06.s1
27	13.8	46.0	41	9	AA976917	AA976917 oc35h041.s
28	13.8	46.0	41	14	H14824	H14824 ym25d07.s1
29	13.8	46.0	49	9	AA410762	AA410762 zc35e11.f1
30	13.8	46.0	49	14	C20874	C20874 HUMGS000494
31	13.8	46.0	49	14	C20875	C20875 HUMGS000494
32	13.8	46.0	49	14	D12406	D12406 HUM007M129
33	13.8	46.0	50	17	A2576739	A2576739 AST--2T007
34	13.6	45.3	37	9	AA934082	AA934082 on27g11.s
35	13.6	45.3	40	9	AA928240	AA928240 on87c07.s
36	13.6	45.3	50	9	AU102621	AU102621 AU102621
37	13.4	44.7	30	14	H41620	H41620 y009b09.f1
38	13.4	44.7	31	14	T78935	T78935 yd21f08.f1
39	13.4	44.7	33	14	N80349	N80349 zai3c12.f1
40	13.4	44.7	35	9	AI801185	AI801185 to79n04.x
41	13.4	44.7	40	9	AI900587	AI900587 sc13c051.y
42	13.4	44.7	44	9	AI494250	AI494250 qy98a01.x
43	13.4	44.7	50	9	AU104332	AU104332 AU104332
44	13.4	44.7	50	17	A2373047	A2373047 1M0125J11
45	13.2	44.0	34	9	AI620509	AI620509 tu56f04.x

ALIGNMENTS

RESULT 1
LOCUS H39590/c
DEFINITION YP01907.r1 Soares breast 3NDBST Homo sapiens cDNA clone
IMAGE:186204 5' similar to gb|U87904|HUMALNE531 Human carcinoma
cell-derived Alu RNA transcript. (rRNA): gb|U81695 LEUCOCYTE
ADHESION GLYCOPROTEIN P150.95 ALPHA CHAIN (HUMAN);, mRNA sequence.
H39590
VERSION H39590.1 GI:915642
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Treviskis, F., Waterston,
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 730
High quality sequence starts: 1

High quality sequence stops: 1
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert Length: 730 Std Error: 0.00
 Seq primer: M13R1
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. 48
 /organism="Homo sapiens"
 /db_xref="GDB:3817100"
 /db_xref="taxon:9606"
 /clone="IMAGE:186204"
 /clone.lib="Soares breast 3MHBst"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: breast; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCATCTGAGTGGAGCGGCCCTTTTCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of a modified pT73 vector (Pharmacia).
 Library went through one round of normalization to a Cot =
 20. Library constructed by Bento Soares and M.Fatima
 Bonaldo."
 BASE COUNT 8 a 10 c 13 g 14 t 3 others
 ORIGIN

Query Match 55.3%; Score 16.6; DB 14; Length 48;
 Best Local Similarity 76.0%; Pred. No. 7.9e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTCATCTGGGTAAAGTGGACAC 25
 1 11 111111 11111 11 11
 Db 37 TCCAGCCTGGTGNAGAGAGAC 13

RESULT 2
 AUI02898/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI02898 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION KAI03269, mRNA sequence.
 ACCESSION AUI02898
 VERSION AUI02898.1 GI:13552419
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMO Rep. 2 (5), 388-393 (2001).
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers

FEATURES

source

1. 50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="KAI03269"

/clone.lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumarate treated U937 cells"
 BASE COUNT 9 a 12 c 16 g 13 t
 ORIGIN

Query Match 54.7%; Score 16.4; DB 9; Length 50;
 Best Local Similarity 76.9%; Pred. No. 9.6e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTCATCTGGGTAAAGTGGACACC 26
 1 11 111111 11 1111 11
 Db 35 TCCAGCCTGGTACAGAGAGAGACC 10

RESULT 3
 AUI06860/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI06860 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION COL03340, mRNA sequence.
 ACCESSION AUI06860
 VERSION AUI06860.1 GI:13556381
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 50)
 AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
 ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
 ,Y., Nakamura,Y., Suyama,A. and Sugano,S.

Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
 ,S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers

FEATURES

source

1. 50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone.lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylfumarate treated U937 cells"
 BASE COUNT 7 a 10 c 11 g 22 t
 ORIGIN

Query Match 54.7%; Score 16.4; DB 9; Length 50;
 Best Local Similarity 76.9%; Pred. No. 9.6e+03;
 Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TTCATCTGGGTAAAGTGGACACC 26
 1 11 111111 11 1111 11
 Db 49 TCCAGCCTGGTACAGAGAGAGACC 24

RESULT 4
 A2796512 48 bp DNA linear GSS 16-FEB-2001
 LOCUS 2M0052H18F Mouse 10kb plasmid UUC1M library Mus musculus genomic
 DEFINITION clone UUC2M0052H18 F, DNA sequence.

ACCESSION A2796512
 VERSION A2796512.1 GI:12944647
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE	Mammalia: Euteleostomi: Eumetazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus.
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel.: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0052 row: H column: 18 Seq primer: CGTTGTAACAGCAGCCGCAT Class: plasmid ends High quality sequence stop: 48. Location/Qualifiers 1..48 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUCG2M0052H18" /clone_1lb="Mouse 10kb plasmid UUCG1M library" /sex="Male" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1473211419b/apf129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT	8 a 10 c 15 g 15 t
ORIGIN	
Query Match	54.0% Score 16.2 DB 17 Length 48;
Best Local Similarity	72.4% Pred No.1.1e+04;
Matches	21: Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY	2 TCATCTGGGTAAAGTGGCACACTGTG 30 Db 12 TCTTTGGGTACATGTGGGCACATGTG 40
RESULT 5	
LOCUS	AUI06864/c 50 bp mRNA linear EST 30-AUG-2001
DEFINITION	AUI06864 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone NBIANZ1NRL, mRNA sequence.
ACCESSION	AUI06864
VERSION	AUI06864.1 GI:13556385
KEYWORDS	EST.
SOURCE	human
ORGANISM	Homo sapiens

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isegaki,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL	EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE	21270072
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES	Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NBLAN21NR1" /clone_lib="Sugano Homo sapiens cDNA library" /note="Differential display comparison of untreated and dimethylflutamate-treated U937 cells"
BASE COUNT	10 a 14 c 15 g 11 t
ORIGIN	
Query Match	53.3%; Score 16; DB 9; Length 50;
Best Local Similarity	79.2%; Pred. No. 1.4e+0; Gaps 0;
Matches	19; Conservative 0; Mismatches 5; Indels 0;
QY	3 CATCTGGGTAAAGAGTGGGACCC 26 28 CAGCTGGCTGACAGAGGGAGACC 5
Db	
RESULT 6	
A1439612	46 bp mRNA linear EST 28-MAR-1999
LOCUS	tcg1b01.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2073481 3'
DEFINITION	Similar to gb:M55531 GALACTOSIDE 2-L-PUCCOSYLTRANSFERASE (HUMAN);, mRNA sequence.
ACCESSION	A1439612
VERSION	A1439612.1 GI:4305543
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 46) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rcgapsb@mail.nih.gov Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever, M.D., Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/TLNL at: www-bio.llnl.gov/btrp/image/image.html
FEATURES	Trace considered overall poor quality Insert Length: 1378 Std Error: 0.00 Seq primer: -40UP from Gbco High quality sequence stop: 1. Location/Qualifiers 1..46

	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:2073481"
	/clone_lib="NCI-CGAP-CLL1"
	/tissue_type="B-cell, Chronic lymphocytic leukemia"
	/lab_host="DH10B"
	/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGAGCGCCGCATGCTTTTTTTTTTTTTTTTTTT
	T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaïdo."
BASE COUNT	18 a 10 c 11 g 7 t
ORIGIN	
Query Match	51.3%; Score 15.4; DB 9; Length 46;
Best Local Similarity	76.0%; Pred. No. 2.3e+04;
Matches	19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db	1 TTCATCCTGGGTAAAGTGGACAC 25 1 TCCAGCCTGGGCACAGAGCAGAC 25
OY	1 TTTCATCCTGGGTAAAGTGGACAC 25 1 1
A1024893/c	A1024893 50 bp mRNA linear EST 27-AUG-1998
LOCUS	ous2b04.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1631407 3'
DEFINITION	similar to contains Alu repetitive element,, mRNA sequence.
ACCESSION	A1024893
VERSION	A1024893.1 GI:3240506
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota:	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 50)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs-rc@mail.nih.gov Tissue Procurement: Christopher Moskalkuk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNML at: www-bio.llnl.gov/bhrp/image/image.html Insert length: 305 Std Error: 0.00 Seq primer: ~40ml3 fwd, EF from Amersham.
FEATURES	Location/Qualifiers
Source	1..50
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:1631407"
	/clone_lib="NCI-CGAP-Br2"
	/sex="Female, pooled"
	/tissue_type="breast"
	/lab_host="DH10B"
	/note="Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT73 vector. This library is the normalized version of NCI-CGAP-Br1.1. Library was constructed by Bento Soares

```

BASE COUNT      12 a      11 c      12 g      15 t
ORIGIN          and M. Fatima Bonaldo. "
Query Match     51.3%; Score 15.4; DB 9; Length 50;
Best Local Similarity 76.0%; Pred. No. 2.4e+04;
Matches        19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY              3 CATCTGGGTAGACTGGGACACCT 27
                ||| | | | | | | | | | | | | | |
Db              43 CAGCCTGGTCAATCATGTAGACACCT 19

RESULT 8
R08290/c       R08290               47 bp    mRNA    linear   EST 05-APR-1995
LOCUS          yllf09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION     IMAGE:127240 3' similar to gb|M87933|HMAAUAU364 Human carcinoma
                cell-derived Alu RNA transcript, (RNA);, mRNA sequence.
ACCESSION      R08290.1
VERSION        R08290.1 GI:760213
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 47)
AUTHORS        Hillier,L., Clark,M., Dubnue,T., Elliston,K., Hawkins,M., Holman
                ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Maiza,M., Parsons,J.,
                Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevisakis,E., Waterston
                ,R., Williamson,A., Wohlmann,P. and Wilson,R.
                The Mashu-Merck EST Project
                Unpublished (1995)
COMMENT        Contact: Wilson RK
                Washington University School of Medicine
                444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel.: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                Insert Size: 716
                High quality sequence starts: 1 High quality sequence stops: 1
                Source: LMG Consortium, LNL This clone is available royalty-free
                through LNL ; contact the LMG Consortium (infoimage.lnl.gov)
                for further information. Trace considered overall poor quality
                Insert length: 716 Std Error: 0.00
                Seg primer: -21ml3
                High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source           1..47
                     /organism="Homo sapiens"
                     /db_xref="GBD:479401"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:127240"
                     /clone_1lb="-Soares fetal liver spleen INFLS"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and spleen; Vector: pTZ193D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     1st strand cDNA was primed with a Pac I - oligo(dT) primer
                     [5' AACTCGAAGAATAATTAAAGATCTTTTTTTTTTTTTTTTTT 3' ],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pTZ193 vector. Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      11 a      13 c      10 g      10 t      3 others
ORIGIN
Query Match     50.0%; Score 15; DB 14; Length 47;
Best Local Similarity 72.0%; Pred. No. 3.4e+04;
Matches        18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```


OY 1 TTCATCTGGGTAAAGAGTGGACAC 25
|||||
Db 26 TTCAGCCTGGGTGAGAGTGGACAC 2

RESULT 9
N38850 35 bp mRNA linear EST 19-JAN-1996
LOCUS YR0611.r1 Soares multiple sclerosis 2NbHMSP Homo sapiens cDNA
DEFINITION clone IMAGE:279884.5' similar to gb|U67933|HUMANLJ064 Human
carcinoma cell-derived Alu RNA transcript, (cDNA); gb|U69556
EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN);, mRNA
sequence.
ACCESSION N38850
VERSION N38850.1 GI:1162057
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
'M., Hultman, M., Kucuba, T., Le, M., Lennon, G., Matis, M., Parsons, J.,
'R., Williams, A., Wohldmann, P., Trevisan, E., Waterston,
'R., Wilson, R., and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: 17
High quality sequence stop: 1.
Location/Qualifiers
1..35
/organism="Homo sapiens"
/db_xref="GDB:3898260"
/db_xref="taxon:9606"
/clone_image="279884"
/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V-type: Phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - Oligo(dT)
primer 15'
TGTACCATCTGAGTGGAGCGCCGATTTTTTTTTTTTTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."

BASE COUNT
7 a 12 c 10 g 6 t

ORIGIN
Query Match 49.3%; Score 14.8; DB 14; Length 35;
Best Local Similarity 73.1%; Pred. No. 3.6e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCTGGGTAAAGAGTGGACAC 26

Db 2 TTCAGCCTGGGTGAGAGTGGACAC 27
|||||
RESULT 10
A2575761 40 bp DNA linear GSS 06-DEC-2000
LOCUS AST-T3280048 Genetrap T47D Human Breast Carcinoma Library Homo
DEFINITION sapiens genomic 5', DNA sequence.
ACCESSION A2575761
VERSION A2575761.1 GI:11562072
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Henkel, G., Liyanage, M., Pratt, E., Huang, D., Riley, M., Bernardino, A.,
'Durick, K., and Pollok, B.
TITLE Exon-trap tags from a T47D Genomescreen(TM) Library
JOURNAL Unpublished (2000)
COMMENT Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel.: 8584048436
Fax: 8584046719
Email: henkel@aurora.bio.com
Pools of cells were isolated from a Genomescreen(TM) library. The
library of cells was generated by retroviral integration of a gene
tagging element consisting of: 1) A promoterless beta-lactamase
proceeded by a splice acceptor as a reporter for gene expression;
2) A promoter driving neomycin resistance followed by a splice
donor to trap downstream exons. 3) RACE from neomycin gene was
performed using total RNA from isolated pools. Output was shotgun
cloned in pAMP-1 and used to transform DH5-alpha competent
bacteria. 5' ends of reported sequences were immediately preceded
by splice donor from the trapping construct.
Class: exon-trapped.
Location/Qualifiers
1..40
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Genetrap T47D Human Breast Carcinoma Library"
/tissue_type="Carcinoma"
/cell_type="Epithelial"
/cell_line="T47D"
/note="Organ: Breast; Vector: pAMP-1; 3' RACE of total RNA
from genetrap pools; shotgun clone in pAMP-1 and used to
transform DH5-alpha competent bacteria."

BASE COUNT
10 a 11 c 11 g 8 t

ORIGIN
Query Match 49.3%; Score 14.8; DB 17; Length 40;
Best Local Similarity 73.1%; Pred. No. 3.8e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 TTCATCTGGGTAAAGAGTGGACAC 26
|||||
Db 5 TTCAGCCTGGGTGAGAGTGGACAC 30

RESULT 11
A2586691 48 bp mRNA linear EST 25-APR-2002
LOCUS A2586691 3'-directed mouse cDNA library Mus musculus
DEFINITION BED0013497 3', mRNA sequence.
ACCESSION A2586691
VERSION A2586691.1 GI:20324496
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 48)
 AUTHORS Kato, K. and Matoba, R.
 TITLE Generation of expressed sequence tags from mouse brain
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5561
 Fax: 81-743-72-5569
 Email: kkatobds.aist-nara.ac.jp,
 URL: http://love2.aist-nara.ac.jp/BED/index.html.
 Location/Qualifiers

FEATURES

source

1. 48

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="BED0013497"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEM-T-easy"
 BASE COUNT 15 a 15 c 7 g 10 t 1 others
 ORIGIN

Query Match 49.3%; Score 14.8; DB 9; Length 48;
 Best Local Similarity 70.4%; Pred. No. 4.1e+04;
 Matches 19; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CATCCGGGTAGAGTGACACCTGT 29
 12 CATCGCTGCTACACAGTGAANCGT 38

RESULT 12
 LOCUS AU108052 50 bp mRNA linear EST 30-AUG-2001
 DEFINITION Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 COL080015, mRNA sequence.
 ACCESSION AU108052
 VERSION AU108052.1 GI:13557574
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki, Y., Tajima, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 'H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 'Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 'S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
 Location/Qualifiers

FEATURES

source

1. 50

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="COLE0015"
 /clone_lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dexamethasone-treated U937 cells"
 BASE COUNT 8 a 11 c 17 g 14 t
 ORIGIN

Query Match

49.3%; Score 14.8; DB 9; Length 50;

Best Local Similarity 73.1%; Pred. No. 4.2e+04;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTCATCTCTGGTAAAGTGGACACC 26
 36 TCCAGCCTGGCAACAGACGAGACC 11

RESULT 13
 LOCUS AI900587 40 bp mRNA linear EST 30-NOV-2001
 DEFINITION sc13c05.y1 Gm-c1013 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 Gm-c1013-513 5' similar to TR:064621 064621 HYPOTHETICAL 82.1 KD
 PROTEIN. ; mRNA sequence.

ACCESSION AI900587
 VERSION AI900587
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Glycine max

REFERENCE 1 (bases 1 to 40)
 AUTHORS Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Corryell, V., Khanna
 'A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
 'Y., Person, B., Smaller, T., Gibbons, M., Page, D., Harvey, N., Schurk
 'R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 'R., Waterston, R. and Wilson, R.
 TITLE Public Soybean EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Shoemaker R./Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand This clone is
 available through: Resgen, Invitrogen Corp. 2130 South Memorial
 Parkway Huntsville, AL 35801 For further information call: (800
)-533-4363 or contact via email: coudresgen.com
 Seq primer: -40RP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1. 40

/organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1013-513"
 /clone_lib="Gm-c1013"
 /tissue_type="whole seedlings, 2-3 week old seedlings,
 greenhouse grown"
 /lab_host="XL10-Gold"
 /note="Vector: pBluescript II XR; site: 1: EcoRI; site: 2:
 XhoI. This cDNA library was constructed from mRNA isolated
 from whole seedlings of 2-3 week old greenhouse grown
 plants. The cDNA library was prepared using the Stratagene
 pBluescript II XR cDNA library construction kit.
 Complementary DNA was synthesized from mRNA using a primer
 consisting of a poly (dT) sequence with a XhoI restriction
 site. EcoRI adapters were ligated to the blunt-ended cDNA
 fragments followed by XhoI digestion. The cDNA fragments
 were directionally cloned into the EcoRI-XhoI restriction
 site of the pBluescript vector. The ligated cDNA fragments
 were transformed into XL10-Gold host cells. This library
 was constructed by Dr. Randy Shoemaker and Dr. John
 Erpelting."
 BASE COUNT 10 a 7 c 17 g 6 t
 ORIGIN

Query Match

48.7%; Score 14.6; DB 9; Length 40;

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